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Result
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MODEL-frame_n2p.model -DEV-xlp
-O-/cgn2_l/USPTO_Spool/US10009782/runat_07052003_122517_23123/app_query.fasta_1.1927
-DB-Swissrot_40 -QFMT-fastan -SUFFIX=rsp -MINNATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-blts -STARF-1 -END-1 -MATRIX=blosum62 -TRANS-human40.cd1 -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_WAT=100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MIXLEN-2000000000
-USER-US10009782_@CGM_1_1_19_@runat_07052003_122517_23123 -NCPU-6 -ICPU-3
-NO_MAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEY_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS-1 -XGAPEXT-0.5 -FGAPOP=6 -FGAPEXT-7
-YGAPPOP=10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Listing first 45 summaries
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NDAD_ALCXX Alcaligenes xylosoxydans xylosoxydans (Achromobacter xylosoxidans). Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae; SEQUENCE FROM N.A., AND PARTIAL SEQUENCE NCBI_TaxID=515;

MEDLINE-96100942; PubMed-8541651; Wakayama M., Katsuno Y., Hayashi S., Miyamoto Y., Sakai K., Moriguchi M.;

"Cloning and sequencing of a gene encoding D-aminoacylase from Alcaligenes xylosoxydans subsp. xylosoxydans A-6 and expression of the gene in Escherichia coli.";
Biosci. Biotechnol. Biochem. 59:2115-2119(1995).
-I- FUNCTION: HAS A WIDE SPECIFICITY; HYDROLYSES N-ACYL DERIVATIVE NEUTRAL D-AMINO ACIDS.
-I- CATALYTIC ACTIVITY: N-acyl-D-amino acid + H(2)0 - an acid + D-

amino acid. COFACTOR: ZINC.

얽

÷ SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE N-ACYL-D-AMINO-ACID DEACYLASE FAMILY.

the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation

EMBL; S80683; AAB35881.1; -. EMBL; D45918; BAA08349.1; -.

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15-JUL-1998 (Rel. 36, I
15-JUL-1998 (Rel. 36, I
                                     STRAIN-A-6;
MEDLINE-93372486; PubMed-7763985;
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                         Moriguchi M., Sakai K., Katsuno Y., 
"Purification and characterization 
amid hydrolase from Alcaligenes xyl
                                                                                                                                                   Alcaligenes xylosoxydans xylosoxydans (Achromobacter xylosoxidans).
Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Achromobacter.
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             Biochem. 57:1145-1148(1993)
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GCGGCCATGCGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCCATCGGCATTTCGACC
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BELONGS TO THE N-ACYL-D-AMINO-ACID DEACYLASE FAMILY.
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                                                    Sakai K., Moriguchi M.;
"Primary structure of N-acyl-D-glutamate amidohydrolase
Alcaligenes xylosoxydans subsp. xylosoxydans A-6.";
J. Biochem. 118:204-209(1995).
                                                                                                                                                                                                                                                                                                                                                                   Alcaligenes xylosoxydans xylosoxydans (Achromobacter xylosoxidans). Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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                                                                                                                                                                                                MEDLINE=96015170; PubMed=8537313;
                                                                                                                                                                                                                                                                    SEQUENCE
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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CATALYTIC ACTIVITY: N-acyl-D-glutamate + H(2)0 = glutamate.
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SUBCELLULAR LOCATION: CYtoplasmic.
SIMILARITY: BELONGS TO THE N-ACYL-D-AMINO-ACID DEACYLASE FAMILY.
                                                                                       GlyPheSerThrGlyLeuAlaTyrGlnProGlyGlyValAlaGluGlnAlaGluLeuAsp
                                                                                                                                                AlaLysGluGlnArgAlaMetGluArgMetLeuAlaAspAlaLeuGluAlaGlyAlaVal
                                                                                                                                                                             GACGAGGAAATCGCGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGCGCCATC
GGCGAGCACATCGTGGCCGCGCTGGAGGAAACCTTCCGCATCGGCCGCGAGCTGGACGTG
                             GlyLeuAlaArgValAlaAlaAlaArgGlyAlaLeuHisThrSerHisIleArgAsnGlu
                                                        GAGGTGTGCCGGCCGCTGAGCGCGCATGGCGGCATCTACGCCACCACGACGACGAA
                                                                                                                   GGCATTTCGACCGGCGCCTTCTACCCGCCGCCGCCGCGCGCCACCGAAGAGAGATCATC
                                                                                                                                                                                                          AspMetAlaMetTyrPheGlyAlaLeuGluAlaGlnArgProMetIleAsnValAlaAla
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P03181;
21-JUL-1986
21-JUL-1986
15-JUL-1998
                  MEDIINE-84270667; PubMed-6087149; Baer R., Bankler A.T., Biggin M.D., De Gibson T.J., Hatfull G., Hudson G.S., Tuffnell P.S., Barrell B.G.; "DNA sequence and expression of the B9 Nature 310:207-211(1984).
                                                                                                                                                                                                                                                                                                                                          1426
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                           Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                                                                    Hypothetical BHLF1 protein.
Epstein-barr virus (strain B95-8) (Human herpesvirus
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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                                                                                                                                                                                                (Rel. 01, Created)
(Rel. 01, Last sequence up
(Rel. 36, Last annotation
                                                                                                                                                                                                                                                         STANDARD;
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                                                          Deininger P.L., Farrell P.J., ., Satchwell S.C., Seguin C.,
                                                                                                                                                                                                                                                       660
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                               Epstein-Barr virus genome.
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626 _. 271	567 AGCCATGGCCAGCGGGCCATCGGCATTTCGACCGGCGCCTTCTACCCGCCCG	B 6
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362 195	303 CACGGTGGTCACGGGCAATTGCGGCATCAGCCTGGCGCCCGCTGGCGCACGCCAACCCGCC	B 5
302 185	243 CGACGACAACTACCTGCTCAGGCGTCGCGACATGACGCCCAAGATCTCGCAGGGCGTCAC.	₿ %
242	183 CACCCGGGTCGACGTGTCGGGCCTGGTGGTCGCCCCGGCTTCATCGACTCGCACACCCA	B 8
182	123 CCTGGGCGTGCGCGGCGACCGCATCGCCGCATCGGCGATCTGTCGGACGCCGCCGCGCA	유 장
122 152	69GCTCGCGGGCGCACCCTCATCGACGGCAGCAACACCCCGGGGGGGG	₽ 5
68 132	39 CCAATCCGATTCCCAGCCCTTCGACCTGCT	무양
	5-10-009-782-1 (1-1758) x YHL1_EBV (1-660)	S.
	ignment Scores: 4.43e-07 Length: 660 ed. No.: 321.50 Matches: 187 ore: 321.50 Matches: 18 rcent Similarity: 31.83% Conservative: 18 st Local Similarity: 29.04% Mismatches: 25 st Local Similarity: 9.75% Indels: 183 ery Match: 1.75% Gaps: 29	Ali Pre Sco Per Per DB:
	EMBL; V01555; -; NOT_ANNOTATED_CDS PIR; A03742; QOBE3: Hypothetical protein; Early proteinomain 149 648 4 X 1 REPEAT 149 273 1. REPEAT 274 398 2. REPEAT 274 398 2. REPEAT 524 648 4. SEQUENCE 660 AA; 66244 MW; 86D	SOTTT
on its no way mmercial	between the Swiss Institute of Bioinformatics and the EMBL outs the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for cc entities requires a license agreement (See http://www.isb-sib.ch/aor send an email to licenseeisb-sib.ch).	8888888

1643 602	1584 TCGCAATACGGCCCCACCCGATATCGTGGGCCAAGGAAGTGATGGGCGGCGCGCGC	4a V9
1583 583	1536 CCCCCTCCCAACCCTGGACGCAAACCGCTACATGGCCCCTCCCTCCGC	ОУ
1535 563	1476 CACGGCCGCCCGGAGCCCGGCGCCAGCCCTTACAATCCGGGGTGAACGGGGCGGCGGCGTGCCG	P Qy
1475 545	1416 CGCGCCGGTCTGGCAAGAGCAGGCGTTCACCGGCCAGCATGCCGGCCG	₽ 2 9
1415 535	TCCGTGTACGTCAACGG -GlyCysProArgThrTrpA	D Qy
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1262 475	1221 GTTCCCGCTGGAGACGGCGGTATGGAAGATGACCGGCCTGAC	Qy Db
1220 455	1182 CCCGCGGGTGCTGGGCCACTATGCGCGCGACCTGGGCCT	ду рь
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1082 396	gagctgcagccggccgccatctacttcatgatgacga AlaalaalaglnargthrHisatgatgProProGlyCys	Qy
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361	918 GGA	d dd
341		g 2
321	GlyThrProAla	을 물
857	TCGGCCGCTCGCGCGAGACGCTGCCGCTGATCGAGGCCGCCATGGC	νQ
797 317	738 AACCTTCCGCATCGGCCGCAGCTGGACGTGCCGGTGGTGATCTCGCACCACAAGGTCAT	Дb
300		B 7
285	sProArgSerAlaArg-AsnProGlyCysProArgThrTrpArg	B B

502	:::::: 93 AlaAlaAlaGlnArg	뮹
776	AGCGGCCGAAATTGGGCCTGGCCCATGACCTTGTGGTGCGAGATCA 7	Qy
9	::: lnGluProArgLeuProGlnAspLeu 4	Ď
36	CTGGCGCGCGATGGCGGCCTCGATCAGC	Qy
472	roSerGlyAlaThrProHisProGluArgGlySerGlyProAlaAsp	Db
869	913TGAGCATGGTGGAGCCGGCCACGTAGGGATACGCGTCCAGCGAGA 8	Qy
452	440 GlyAlaProGlyThrProAlaAlaProGlyProGlyGly 4	
914	970 GGAAGGGCTTGCACCAGGTGATGATGGTGCGTCCGGCCAGCAGCACGCGGTCCTGCT 9	Qy
439	420 ProProProGlyAlaGlyGlnArgProSerGlyProThrGlyGlyArgProAlaAlaPro 4	뮍
971		Qy
419	TrpArgArgArgSerGlyAlaGlnArgGlyH1s	망
1031		Qy
399	383 GlyAlaAlaGlnArgThrHisArgArgProProGlyCysProArgSer :	Вb
1088		Qγ
382	.363 LeuProGlnAspLeuAlaAlaGlnArgCysProAlaGlyProProProThrArgSer	Db
1148	TCGT	VΩ
362	343 SerGlyProAlaAspProProAlaAlaAlaArgLeuProProGluArgGlnGluProArg	В
1193	TGCCCCA	Qy
342	323 ProGlyProGlyGlyAlaAlaValProSerGlyAlaThrProHisProGluArgGly	밁
1223	ATCTTCCATACCGCCGTCTCCAGCGGGA	Qγ
N	 oGlyAlaProGlyThrProAlaAla	В
1283	TACCCGGCCTGCAGCTGCCCGCGCCCCGG	Qy
302	 lyAlaGlnArgGlyHisProProProGlyAlaGlyGlnArg	망
1328		Qy
282	 CysProArg	₽
1364	GAATGGATGCCGGCGCGCGCTCGGTAGGGTGTTCGA	Qy
262	SerGlyAlaAlaAlaGln	뮍
1418	26	Qy
242	roArgLeuProGlnAspLeu	DЪ
1457		Qy
222	lyAlaThrProHisProGluArgGlySerGlyProAlaAsp	뮰
1481	CGTTCACGCCGGATTGTAAGGGCTGGCGCCCGGGCTCAGGCGG	Qy
206	AlaProGlyAlaProGlyThrProAlaAlaProGlyProGlyGlyGlyAlaAlaVal	밁
1535	CCAGGGTTGGGAGGGGGC	Qy
186	167 ArgGlyH1sProProProGlyAlaGlyGlnArgProSerGlyProThrGlyGlyArgPro	밁
1559	AGGGAGGGCCATGTAGCGGT	Qy

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STRAIN-S288C / AB972;
Barrell B.G., Badcock K., Bankler A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.,
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
[2]
                                                                                                                                                                                                                                                                                                                               P08640; F08068;

O1-AUG-1988 (Rel. 08, Created)
O1-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glucoamylase S1/S2 precursor (EC 3.2.1.3) (Glucan glucosidase) (1,4-alpha-D-glucan glucohydrolase).
STA1 OR STA2 OR MAL5 OR YIRO19C.
                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Saccharomyc
                                                                                                                                                                                                                                                    Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                          SEQUENCE FROM N.A
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                              Ser Ser A La {\tt ProValThrSerSerThrThrGluSerSerAlaProValProThr}
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluSerSerSerAlaProAlaProThrProSerSerSerThrThr------Glu
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                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                  entities requires a license agreement or send an email to license@isb-sib.ch
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;
FleisChmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                        Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekkia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                            laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: BELONGS TO THE N-ACYL-D-AMINO-ACID DEACYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q10830;
01-OCT-1996
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STRAIN-H37Rv;
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15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein Rv2913c.
RV2913C OR MT2981 OR MTCY274.45C OR MTCY338.01C.
                                                                                                                                                                                                                                                     Whole genome comparison of Mycobacterium tuberculosis
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                                                          an email to license@isb-sib.ch;
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Scores: 6.28e-06 Matches: 29.40 Matches: 153 Similarity: 36.48 Conservative: 216 Mismatches: 216 Mismatches: 216 Mismatches: 216 Mismatches: 216 Mismatches: 217 Mismatches: 216 Mismatches: 216 Mismatches: 216 Mismatches: 216 Mismatches: 217 Mismatches: 216 Mism	816 CCGCTCGCGC :: 279 nArgArgLysGlyVa	56 CGAGCTGGACGTG ::::: 60 -AspValAspAsn	696 CATGCGCGACGAAGGCG ::: 245 IleSerValLeuArg	648CGAG 225 ArgPheArgSerArgA	595 TCGACCGGCGCCTTO	535 GAAATCGCGGCCATO	493 GCCGCGGTCATGCCC	433 TTGCGGGCCACGCCGGCGGCCG :::	391GGCTCTTACCGT	52 GCC 13 Ala	292 CAGGGCGTCACCAC 	232 TCGCACACCCACGA 	172 GCCGCCGCGCACAC 56 ThrGlyCysProGl	8 GCCG	6 8	-10-009-782-1 (1-1758)	nment Scores: . No.: e: Ent Similarity: Local Similarity: y Match:
GGGCGGCGC ProLeuThr CTGTCGGAC ::: LeuAspGlu TTCATCGAC ::: LeuAspGluPhe PhelleAsp AAGATCTCG :::: ThrValTyr ThrValTyr TheGluPhe CTGGACGCG ::::: ::: LeuGlyMet ATCGCACCA ::: LeuGlyMet ATCGGCACCA ::: LeuGlyMet ATCGGCACCA ::: LeuGlyMet ATCGGCACCA ::: LeuGlyMet ATCGGCACCA ::: LeuGlyMet ATCGGCACCA ::: LeuGlyMet ATCGGCACCA ::: LeuGlyMet ATCGGCACCA ::: LeuGlyMet ATCGGCCCCA ::: LeuGlyMet ATCGGCCCCA ::: LeuGlyMet ATCGGCCCCA ::: LeuGlyMet ATCGGCCCCA ::: LeuGlyMet ATCGGCCCCA ::: LeuGlyMet ATCGGCCCCA ::: LeuGlyMet ATCGGCCCCA ::: LeuGlyMet ATCGGCCCCA ::: ATTCGGCCCCA 	largMetSerMetLeuValSerAlaAs	TGATCTCGCACCACAAGGTCAT ::: eralaLeuLeuPhePheLeuAl	AGCACATCGTGGCCGCGCTGG HisargGlyArgIle	<pre>3TGTGCCGGCCGCCTGAGCGCGC ::: ::: laLeuProSerThrPheAlaTh</pre>	ACCCGCCGCCGCCGCCAC	GCGGGACCTGGCCGAGGAAGCCATGGCC; 	GCGGTCATGCCGGACTTGCAGCGCGCCGCC ::: AlaValLeuGlyLeuAspArgAlaThrAspAspThr	GGCCG uGlyF	ָי בַּק	GGACCTGCTGGACGAAGGC aAspLeuPheSerArgVal	GCGTCACCACGGTGGTCACGGGCAATTGCGGCATCAGC ::: 1.yValThrThrValLeuLeuGlyAsnCysSerLeuSer	CGACAACTACCTGCTCAGGCGTCGCGAC raspalaGluValLeuLeuAspProGly	CCGGGTCGACGTGTCGGGCCTGGTGGTC ::: 	GCCGACCTGGGCGTGCGCGGCGGCGCATCGCCGCC ::: ArgThrLeuGlyIleArgAspGlyValValAlaThrValAla	GAC Asp	_мусто (1-611	8e-06 Length: .00 Matches: 488 Conservative 06% Mismatches: Indels: Gaps:
	GA	GGGCCAGCCCAATTTCG aSerSerArgIlePheA	GCATCGGCC nSerAlaPr	ATCTACGCCAC	\T \spGlyAs	ATCGGC ::: LeuGly	ACCGACG ::: ArgProThrGluA	GGCCATTCAACGCTGCGC GlyHisSerAspLeuArg	GCCGACTACCTGGACGCG	aValProArgGluF	méececce	CCCAAGATCTC ;;; GluSerValAr	GGCTTC GlyPhe	TCGG : AspG	ACACCCGGGGGGGG		N H N Z H O

	LT 8 _HUMAN MUC2_HUMAN STANDARD; PRT; 5179 AA. Q02817; Q14878;	.29	RES MUC ID AC	
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597		1487	\$ E	
148	CATGCCGGCCGCGTGC	· ·	. Q	
584	alValAlaThrGlyValGlyGlyThrValValPheArgGlyGlyGlnPheGlyGlyGlnP	564	탕	
145	TCCATTCCGTGTACGTCAACGGCGCGCGCGGTCTGGCAAGAGCAGGCGTTCACCGGCCAG-	1394	Qy	
564	. luGluAlaValProTyrTyrGlyGlyLeuArgArgMetValAsnArgAsnAspAlaThrV	544	B	
139	CT	1373	Qy	
544		524	рь	
137	acegteeccatacceccaccttcgaaca	1313	Qy	
524	hrGlyGluLeuAlaGluTrpPheGlyIleGlyAlaGlyThrLeuArgGlnGlyAspA	505	밁	
131	CCGGCCTGACCGCCGCGCGCGCTTCGGCCTGGCCGGGCGCGGGCAGCTGCAGGCCGGGTA	1253	Qy	
505	rgAspAlaAspArgAlaGlÿGlnProPheLeu	485	рb	
125	:	1225	Ωy	
485	::: ::::::::::::::::::::::::::	465	Дb	
122		1196	Qy	
465		445	Дb	
119	TGCCGCACGACGAGCGCCCGCATCCGCGCCTGTGGGGCACCTTCCC	1139	Qy	
445		429	g D	
113	ACGAACCCGACGTGCAGCG	1079	γQ	
429	 	416	밁	
107	GTACGACGTGGTGCCGAGCTGCAG	1026	Qy	
415	OASpLysSerLeuIleGlyLysSerPheGlyAlaIleAlaAspGluArgGly	398	Db	
102	CTTCCCCGAACTGAGCGGGCGCGACCTGGATGAAGTCGCGGCCGAGCGCGG	966	Qy	
398	::: 	379	뫄	
965	ATCATCACCTGGTGCAAG	946	Qy	
379		359	탕	
945	CGTGCTGCTGGCCGGACGCAC	924	Qy	
359		339	Db.	
923	CCCTACGTGGCCGGCTCCACCATGCTCAAG	988	Ωу	
339		319	Db	
885		849	Qγ	
319	 AlaValHisValPheGlyLeuGlyThrArgValLeuAsnLysLeuLeuGlySerGlnVa	299	Дb	
848	GATCGA	840	Qy	

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InterPro; IPRO00359;
InterPro; IPRO024061;
InterPro; IPRO024061;
InterPro; IPRO02919;
InterPro; IPRO01007;
InterPro; IPRO01846;
                                                                     EMBL; M74027; AAA5;
EMBL; M94131; AAA5;
EMBL; M94132; AAA5;
Genew; HGNC:7512; MMIM; 158370;
                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                  and
                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1343-1895 AND 4176-4195 FROM N.A. MEDLINE-91358717; PubMed-1885763; Toribara N.W., Gum J.R. Jr., Culhane P.J., Lagace R.E., Hicks J.W., Petersen G.M., Kim Y.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Intestine;

MEDLINE-94132002; PubMed-8300571;

Gum J.R. Jr. Hicks J.W., Toribara N.W., Siddiki B., Kim Y.S.;

"Molecular cloning of human intestinal mucin (MUC2) cDNA.

Identification of the amino terminus and overall sequence simito prepro-von Willebrand factor.";

J. Biol. Chem. 269:2440-2446(1994).
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"The human MUC2 intestinal mucin has cysteine-rich subdomains loca both upstream and downstream of its central repetitive region."; J. Biol. Chem. 267:21375-21383(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mucin 2 precursor (Intestinal mucin 2).

MUC2 OR SMUC.
HOMO sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                        MUC-2 human small intestinal mucin gene structure.
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01-NOV-1997
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15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                     polymorphism.";
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           )1846; VWF_D.
Cys_knot; 1.
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                          : Cys_knot.
: EGF-like.
: GF_cysknot.
: TIL_Cysrich.
: VWF_C.
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35, Last sequence update)
41. Last annotation update)
(Intestinal mucin 2).
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ŧ	GCGGGACCTGGCCGAGGAAGCCATGGCCATCGGCATTTCGACCG 601	01 SerProPr	d da
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	-1758) x MUC2_HUMAN (1-5179)	10-009-782-1 (1	-Sn
	8.01e-06 Length: 5179 289.50 Matches: 146 32.92% Conservative: 41 1ty: 25.70% Mismatches: 164 8.78% Indels: 217 1 Gaps: 29	Alignment Scores: Fred. No.: Score: Score: Percent Similarity Best Local Similar Duery Match:	All Pre Sco Per Bes Que DB:
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09 842 TOCAGGCCCCANGGCCGCCAGGACGCCCTCCACCGCTACCCCT ACCTGGCCG 938 Db 1549						
842 TGAGGCCGCCATGGCGCCACAGACGTCTCCCGTTCACCTTTCACTTTTTTTT	7,	Db Db		0 dq		40 40 40 40 40 40 40 40 40 40 40 40 40 4
3 5 4 5 7 5 9 9 7 7 6 8 3 3 7 2 1 6 6 8 1 1 7 8 6 8	VALPRYKA VNUA_PRVKA VNUA_PRVKA STANDARD; PRT; 1733 p33485; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence updat 01-FEB-1994 (Rel. 28, Last annotation upd Probable nuclear antigen. Pseudorables virus (strain Kaplan) (PRV). Viruses; dsDNA viruses; no RNA stage; Her Alphaherpesvirinae; Varicellovirus. NCBI_TaxID=33703; [1]	1526 CGGCGTGCCGCCCCCCAACCCTGGACGCAAACCGCTACATGGCCCCTCCCCTCCGCTC 1 1745 ThrThrLeuProProThrThrThrSerSerProLeuThrThrThrProLeuProPro 1 1586 GCAATACGGCCCCACCGATATCG 1609 :::	1388	1634	1585 ThrProSerProProThrIleThrThrThrThrThrThrThrThrThrThrThrThrThrT	842 TCGAGGCCGCCATGGCGGCCAGGACGTCTCGCTGGACGCGTATCCCTACGTGGCCG 1549ProProThrSerThrThrThrLeuProProThrThrThrPro 899 GCTCCACCATGCTCAAGCAGGACCGTGCTGCTGCTGGCCGACCATCATCACCTGGT

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945 GlyArgAlaAlaLeuLeuAlaProLeuGlyArgTrpValArgAlaGlyGlyGlyGly 964
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Virology 179:365-377(1990).
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P21561;
01-MAY-1991
01-MAY-1991
16-OCT-2001
122 AspArgArgAlaProGlyValAspSerArgLeuArgGlnGlnHisGlnHisProArg---
                               192 CGACGTGTCGGGCCTGGTGGTCGCCCCGGCTTCATCGACTC---GCACACCCACGACGA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M38373; -; NOT_ANNOTATED_CDS.
PIR; C39135; C39135.
Hypothetical protein.
SEQUENCE 437 AA; 50626 MW; B5B9
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the European Bioinformatics Institute.
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                                                                                                  147 CGCCGCCAT-----CGGCGATCTGTCGGACGCCGCCGCGCA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haloferax sp. (strain Aa 2.2).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Haloferax.
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01-MAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mypothetical 50.6 kDa protein in the 5'region of GYRA and GYRB (ORF
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                                                               ArgArgHisLeuLeuArgArgArgValGlyGlyH1sArgGlyArgAsnArgHisAlaGly 121
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 ArgGlySerThrAlaAlaValProArgProLeuProArg
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                                                   AlaAlaTyrAlaSerValPro---AlaHisAlaProAlaHisArgGlyArgLeuArgVal
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Vleek C., Kozmik Z., Paces V., Schirm
"Pseudorabies virus immediate-early go
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Pseudorables virus (strain Kaplan) (PRV).
Viruses; daDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=33703;
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652	08 TICGICGCGATGIGGGIGGCGIAGAIGCCGCCAIGCGGCGCCICAGCGGCGCACA	Qy 7
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1048	GTCCGGCCAGCAGCACGCGTCCTGCTTGAGCATGGTGGAGCCGGCCACG	0y 10
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1006	65 GATGGCGCCGGCCGGCTGCAGCTCGGGCACCACGTCGTACTTGGATTTGCCGCGCCTCC	_
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11	CGTCTCCAGCGGGAACAGGCCCAGGTCGCGCGCATAGTGCCCCCAGCACCCGC	Qy 1
93	alAlaValProAlaGluGlyArgAlaGlyGlu-ProLeuValLeu-	В
12	281CAGGCCGAAGCGCGCGGCGGTCAGGCCGGTCATCTTCC	Qy 1
1 916	98 SerGlyProGluSerGluGlyAlaAlaLeuAlaProGlyProProValLeuPheVa	9
,	GAAGTACCCGGCCTGCAGCTGCCCCCCCCCCCCCCCC	Qy 1
AG 1321 :: Tq 897	74	B 5
ro 877	ASPALAALaGluAlaAlaValGlyArgGlyValLeuGlyHisGlyProGluArgAlaF	2 6
- 1372	395 GATGCCGGC	. Qy
g 857	845 ArgLeuGlyGlyPro	
3 13	FGACGTAC	Qy
C 1456	515 GCCGGATTGTAAGGGCTGGCGC	B 25
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SEQUENCE OF 1-181 FROM N.A.
SEQUENCE-84270697; PubMed=6462220;
Chu M.-L., de Wet W.J., Bernard M.P.
Myers J., Williams C., Ramirez F.;
"Human pro alpha 1(I) collagen gene
conservation of a pattern of introns
Nature 310:337-340(1984).
                                      FASEB
                                                                                                REVIEW ON VARIANTS.
MEDLINE-91184577; PubMed-2010058;
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[9]
SEQUENCE OF 1-44 FROM N.A.
Company of the compa
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   REVIEW
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"Isolation and characterization of the che alpha 1 and alpha 2 chains of human Biochemistry 9:4699-4706(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-88124208;
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Morgan P.H., Jacobs H.G., Segrest J.P., Cunningham
"A comparative study of glycopeptides derived from
vertebrate collagens. A possible role of the carboh
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LINE-85130970; PubMed-2857713;
M.-L., de Wet W.J., Bernard M.P., For structural analysis of the human moter structure, Alul repeats, and Facility of the Medical Chem. 260:2315-2320(1985).
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ae J.K., Raassina M., Virta
pro alpha 1(I) collagen: cl
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enhance transcription.";
. 262:15151-15157(1987).
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VARIANTS
                        Marini J.C., Grange D.K., Gottesman G.S., Le "Osteogenesis imperfecta type IV. Detection one alpha 1(I) collagen allele (CCLIAI) by I J. Biol. Chem. 264:11893-11900(1989).
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MEDLINE-89308591; PubMe
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chain in lethal perinatal osteogenesis imp
the peptide defect by in vitro expression
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MEDLINE-89255493; Publ
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MEDLINE-88033031; PubMed-3667599;

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MEDLINE-8722295; PubMed-3108247;

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MEDLINE-86287390; PubMo
Cohn D.H., Byers P.H.,
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"Mutations in fibrillar collagens (types I, II, III
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MEDLINE-97169389; PubMed-9016532;
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J. Med. Genet. 28:433-442(1991).
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osteogenesis imperfecta resulting from a single
in one human pro alpha 1(I) collagen allele.";
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472 ArgGlyGluProGlyProThrGlyLeuProGly---ProProGlyGluArgGlyGlyPro 490
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                                  396 TTACCGTTTCGAGCGCTTCGCCGACTACCTGGACGCGTTGCGGGGCCACGCCGGCGGCCGT 455
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thermal stability are either position of amino acid specific.";
J. Biol. Chem. 264:19694-19699(1989).
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Lamande S.R., Dahl H.-H.M., Cole W.G., Bateman J.F.;
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COLIA2 genes causing lethal perinatal osteogenesis imperfecta.";
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                NONHELICAL REGION (N-TERMINAL).
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Db 404 ProGlnGlyLeuAlaGlyLeuGlnGlyArgAlaGlyProProGlyAlaArgGlyGluPro	CATCGACTCGCACACCACTOTTCTYFTOGIT	388 GlylleArgGlyLysAspGlyLysGlnGlvGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG	144	368	Ov 102	Db 348 ProglyAlaLysglyPromhrglyAsamhan	338 1	3 ATTCCACTTGATCGCGGAAGGAGAGATTTCCATGTCCCAATCCGATTCC	US-10-009-782-1 (1-1758) x CAFF_RIFPA (1-1027)	1 Gaps:	Agron: March: 8 17% Conservative: 48 March: March: 8 17% Mismatches: 22	6.34e-05 Length: 269.50 Matches:	gnment Scores:	903 P -> A.	MOD_RES 1019 1019 . MOD_RES 1020 1020	MOD_RES 1017 1017	1014 1014	MOD RES 1013 1010	RES 990 HYDROXYLATION.	MOD_RES 966 966 MOD_RES 984 984	MOD_RES 954	MOD_RES 939 939 MOD_RES 945 945	915 HYDROXYLATION. 915 HYDROXYLATION.	MOD_RES 894 894	MOD_RES 867 867	MOD_RES 855 855	MOD_RES 843 HYDROXYLATION.	MOD_RES 815 815	MOD_RES 783 HYDROXYLATION. MOD_RES 783 HYDROXYLATION.	MOD_RES 774 774	MOD_RES 723 723 MOD_RES 744 744 MOD_RES 750 750	714 717	MOD_RES 708 708 MOD_RES 711 711	648 648 . H	647 647
LuPro 423	G1y 403		rgPro 387	GACCG 143	roGly 367	101	lyGlu 347	TTCGA 62	· · · · · · · · · · · · · · · · · · ·																										
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660 IleGlyPheProGlyGluArgGlyThrArgGlyAlaThrGlyLysGlnGlyAlaArggly 679		640 GIVILEGINGIVENDE CONTROL OF THE				1080 CGAACCCGACGTGCAGGCCATGCTGGGCCTTCGGCCCGACGACGACGGCCT 1139	588ArgGlyLysAspGlyGluArgGlyGluArgGlyGluAsnGlyLeuProGly 604		573***GlySerArgGlyAspIleGlyProArgGlyLysAlaGlyGlu 587	* * JOSOPO SA SOLOSO		OO CTCCACCATGCTCAAGCAGGACCGCGTGCTGCTGGCCGGACGACCATCATCATCATCATCATCATCATCATCATCATCATCA			Alaciverombroi	780 CTCGCACCACAAGGTCATGGGCCCAGCCCAATTTTTTTTT		720 CGTGGCCGCGGGAGGAAACCTTCCGCATCGGCCGCGAGCTGGAGCTTGGACGTTCCCCCTTTTTTTT			522	600 CGGCCCTTCTACCCGCCCGCCCGCCCACCACCAAGAGAGATCATCGAGGTGTGTGCCC	516	540 CGCGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCATGGCCATCATCATTTTTCATTTTCATCATTTTTCATCATTTTTCATCA	501SerGlyProAlaGlyProGlyGlyGlyAlaproClyAla	480 TICAACGCIGCGCGCGCGCGCCAGGTCATGCCACTTTTTTTTTT	482	420	462	360 GCC	444AspGlyGluThrGlyAlaAlaGlyProProGlyAlaAlaGlaTingscompacto	300	A . A	3	

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Campbell B.G., Wootton J.A.M., McLeod J.N., Minor R.R.;
Sequence of normal canine COLIA1 cDNA, ";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

I- FUNCTION: TYPE I COLLAGEN IS A MEMBER OF GROUP I COLLAGEN

SUBMIT: TRIMERS OF ONE ALPHA 2(I) AND TWO ALPHA 1(I) CHAINS.

UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

UNIT (G-X-Y) CONTAINS 1 VWFC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1686 GGCCAGCGGCATCGCGGTCTCGACCCTGTCCAAGGCCGAGCTGGGCCAGATCGCCCT 1742
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Canis.
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Best Local Similarity:
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       555 aGlyGlnAspGlyArgProGly-
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00038; COLFI; 1. SMART; SM00214; VWC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01391; Collagen; Pfam; PF01410; COLFI; 1.
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                              GGCATTTCGACCGGCGCCTTCTACCCGCCCGCCGCCGCGCGCCACCA------
                                                         euThrGlySerProGlySerProGlyPro--AspGlyLysThrGlyProProGlyProAl
                                                                                       GACGAGGAAATCGCGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCATC
                                                                                                                     --GlySerProGlyGluAlaGlyArgProGlyGluAlaGlyLeuProGlyAlaLysGlyL
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31.92%
27.70%
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TRIPLE-HELICAL REGION.
NONHELICAL REGION (C-TERMINAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-S8E3674D2B570697 CRC64;
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COLLAGEN ALPHA 1(I) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
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Matches:
Conservative:
Mismatches:
-ProProGlyProProGlyAlaArgGlyGl
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ROCCORPIN

Canis familiaris (Dog). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;

30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Collagen alpha 1(I) chain precursor.

Q9XSJ7; 30-MAY-2000 CA11_CANFA

STANDARD;

PRT;

1460 AA.

823

GlyGluArg-----

TISSUE-Skin SEQUENCE FROM N.A.

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1626

813 GlyGlyProPro

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793

1569

1509

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Takeuchi, K., Koide, Y., Hirose, Y., Moriguchi, M. and Isobe, K.

Transformed microorganism and process for producing D-aminoamylase Patent: JP 2001000185-A 1 09-JAN-2001;

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	CCTTACAATCCGGCGTGAACGGGGCGGCGTGCCGCCCCCCCC	1501 c	DЬ
1560	CCTTACAATCCGGCGTGAACGGGGGGGGGCGTGCCGCCCCCTCCCAACCCTGGACGC	501	Qy
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32	TGGTGGTGTTCGACCCGGCCACGGTGGCCGATACCGCCACCTTCGAACACCCTACCGA	1321	Qy
132	ACCGCCGCGCGTTCGGCCTGGCCGGGCGCGGCAGCTGCAGCCGGGTACTTCGCCGAC	1261	ДD
132	CGCCGCGCGCTTCGGCCTGGCCGGGCGGCGGCAGCTGCAGGCCGGGTACTTCGCCGA	1261	Qγ
26	TATGCGCGCGACCTGGGCCTGTTCCCGCTGGAGACGGCGGTATGGAAGATGACCGGCCTV	1201	D.
126	ATGCGCGCGACCTGGGCCTGTTCCCGCTGGAGACGGCGGTATGGAAGATGACCGGCCT	1201	ν
20	CGCACGACGACGCCCCCATCCGCGCCTGTGGGGCACCTTCCCGCGGGTGCTGGGGCAC	1141	g
120	CGCACGACGAGCGCCCGCATCCGCGCCTGTGGGGCACCTTCCCGCGGGTGCTGGGGCCA	1141	Qy
14	GAACCCGACGTGCAGCGCATCCTGGCGTTCGGCCCGACCATGATCGGCTCCGACGGCCT	1081	DЪ
11	AACCCGACGTGCAGCGCATCCTGGCGTTCGGCCCGACCATGATCGGCTCCGACGGCC	1081	Qy
<u>, , , , , , , , , , , , , , , , , , , </u>	TCCAAGTACGACGTGCTGCCCGAGCTGCAGCCGGCCGGCC	1021	Db.
10	CCAAGTACGACGTGGTGCCCGAGCTGCAGCCGGCCGGCGCCATCTACTTCATGATG	1021	Qy
10	AGCCCTTCCCCGAACTGAGCGGGCGCGACCTGGATGAAGTCGCGGCCGAGCGCGGCAAA	961	Д
10	GCCTTCCCCGAACTGAGCGGGGGGGGGACCTGGATGAAGTCGCGGCCGAGCGCGGG	961	Qy
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י סי	CCACCATGCTCAAGCAGGACCGCGTGCTGCTGCTGGCCGGACGCACCATCATCATCACCTGCT	901	Qy
၀ - ၂ ၂	ATCGAGGCCGCCATGGCGCCCAGGACGTCTCGCTGGACGCGTATCCCTACGTGGCCGG	841	ДĎ
90	TCGAGGCCGCCATGGCGCCCAGGACGTCTCGCCTGGACGCGTATCCCTACGTGGCCG	841	Qy
16 840			Дb
, ,	CGCACCACAAGGTCATGGGCCAGCCCAATTTACACACACA	781	γQ
7 - 6		721	DЬ
7 7 7	TGGCCGCGCTGGAGGAAACCTTCCGCATCGGCCGCGAGCTGGACGTGCCGGTGGTG	721	γQ
72	CGCTGAGCGCGATGGCGGCATCTACGCCACCCACATGCGCGAGGAAGGCGAGCACAT	661	망
72	CGCTGAGCGCGCATGGCGGCATCTACGCCACCACATGCGCGACGAAGGCGAGCAC	661	Qy
5	GCCCCTTCTACCCGCCGCCGCCCCCCCCCCCACGAAGAGATCATCGAGGTGTGCCC	601	ДЪ
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	GCGCCTTCTACCCGCCGCCGCCGCGCGCCACCGAAGAGATCATCGAGGTGTG	601	Qy
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                                                                                                                                                                              Takeuchi K., Koide Y., Hirose Y., Moriguchi M., Isobe K.; "Transformant microorganism and process for producing D-aminoacylase"; Patent number JP03074329-T/1, 12-JAN-2001.
AMANO PHARMACEUTICAL CO LTD.
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         15-JUN-2000 JP 2000003932
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KENICHI TAKEUCHI, YOSHINAO KOIDE, YOSHIHIKO HIROSE,
MITSUAKI MORIGUCHI,
                                                                                                                                                                                                                                                                         Alcaligenes xylosoxydans subsp. xylosoxydans
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AUTHORS
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dan-D-aminoacylase [Alcaligenes
A-6, Genomic, 1980 nt]
                                                  GenBank staff at the National Library of Medicine created this entry (NCBI glbbsq 174864) from the original journal article. This sequence comes from Fig. 3.
                                                                                               Alcaligenes xylosoxydans subsp. xylosoxydans the gene in Escherichia coli Biosci. Biotechnol. Biochem. 59 (11), 2115-21
                                                                                                                          Cloning and sequencing of a gene encoding D-aminoacylase from
                                                                                                                                          Wakayama, M., Katsuno, Y., Hayashi, S., Moriguchi, M.
                                                                                                                                                                                       Achromobacter xylosoxidans A-6 Achromobacter xylosoxidans
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Y (bases 1 to
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CCGCTGAGCGCGCATGGCGGCATCTACGCCCACCATGCGCGACGACGAAGGGCGAGCACATC
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/TTABS18 tion-"MOSDISQPFDLILLAGGTLIDGSNTPGRRADIGVRGDRIAAIGDL
SDAAAHTEVDLIDLEGGSYRFERFADYLDALBATPAAVNAACMYGHSTLRAAVMPDL
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QRAATDEELAAMEDLAEERAMASGA IGISTGAFYPPAARATTEELIEVCRPLIEAAMAR
ATHMRDEGEHIVAALEETFRIGRELDVPVVISHKYNGQPNTGRSRETLLEAAMAR
AUVSLDAYPYAGSTMLKQDRVLLAGRTIITWCKPFPELSGRDLDEVAAERGKSKYDV
VPELQPAGAIYFMUNGDFDVQRILLAFGPTMIGSDGLPHDERPHRLWGTFPRVLGHYAR
DLGLFPLETAVMKNTGLTAAARFGLAGRQCLAGAYFADLVVFDPATVADTATFEHPTER
AAGIHSYVYNGAPVWQDQAFTGQHAGRVLARTAA"

AAGIHSYVYNGAPVWQDQAFTGQHAGRVLARTAA"

AAGIHSYVYNGAPVWQDQAFTGQHAGRVLARTAA"
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/protein_id-"AAB35881.1"
/db_xref-"GI:1488357"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cloning and sequencing of a gene encoding D-aminoacylase from Alcaligenes xylosoxydans subsp. xylosoxydans A-6 and expression the gene in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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Primary structure of N-acyl-D-glutamate amide alcaligenes xylosoxydans subsp. xylosoxydans
J. Blochem. 118 (1), 204-209 (1995)
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Alcaligenes xylosoxidans DNA for N-acyl-D-amino acid
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VPELOPAGAIYEMMDEPDVQRILAFGPTMIGSDGLPHDERPHPRLWGTFPRVLGHYAR
DLGLFPLETAVWKMTGLTAARFGLAGRGGLQAGYFADLVVFDPATVADTATFEHPTER
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/protein_id="BAA08349.1"
/db_xref="GI:1881397"
/db_xref="GI:1881397"
/db_xref="GI:1881397"
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SDAAAHTRVDVSGLVVAPGFIDSHTHDDNYLLRRRDMTPKISOGVTTVVTGNCGISLA
PLAHAMPPAPLDLLDEGGSYRFERFADYLDALRATPAAVNAACMVGHSTLRAAVMPDL
QRAATDEEIAAMRDLAEEAMASGAIGISTGAFYPPAARATTEEIIEVCRPLSAHGGIY
ATHMRDEGEHIVVAALEETFRIGRELDVPVVISHKVNGOPNTGRSRETLPLLEAAMAR
ATHMRDEGEHIVVAALEETFRIGRELDVPVVISHKVNGOPNTGRSRETLPLLEAAMAR
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/sub_species="xylosoxydans"
/db_xref="taxon:85698"
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           Score 1453.4;
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                                                        GATGAAGTCGCGGCCGAGCGCGAATCCAAGTACGACGTGGTGCTGCCGAGCTGCAGCCG
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         GGCACCTTCCCGCGGGTGCTGGGGCACTATGCGCGCGACCTGGGCCTGTTCCCGGCTGGAG
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Similarity

61.9%; nilarity 84.3%; Conservative

Score 1088.6; DB 1; Pred. No. 6.6e-110; 0; Mismatches 229;

Indels Length

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ATGTCCCAATCCGATTCCCAGCCCTTCGACCTGCTGCTCGCGGGGGGGCACCCTCATCGAC 93

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BASE COUNT
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Alcaligenes :
Bacteria; Pro
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Submitted (28-DEC-2000) Institute of Biochemistry, National Submitted (19-DEC-2000) Institute of Biochemistry, National Yang-Ming University, 115, Li-Nong St. Sec. 2, Shih-Pai, Taiwan 11221, R.O. China
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Hsu,C.S., Lai,W.L., Chang
Gene cloning, nucleotide;
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Alcaligenes faecalis D-aminoacylase
AF332548
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                                                               /TLANS18110VACKVVSPGFIDSHTHDDNYLLKHRDMTPKISQGVTGVRGDRIAAVGDL
SASSARRIDVACKVVSPGFIDSHTHDDNYLLKHRDMTPKISQGVTTVVTGNCGISLA
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REATADEIGAMQALADDALASGA IGISTGAFYPPANAASTEEIIEVCRPLITHGGVY
ATHMRDBGEHIVQALEETFRIGRELDVFVVISHKYNGKLNIFGRSKETLALIEAAMAS
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VPELQPAGA IXTMMZDEPDVQRILAFGFTMIGSDGLFHDERPHRLMGTFPKYLGHTSR
VPELQPAGA IXTMMZDEPDVQRILAFGFTMIGSDGLFHDERPHRLMGTFPKYLGHTSR
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AAGIHSYYVNGAAVWEDQSFTGQHAGRYLNRAGA"

AAGIHSYYVNGAAVWEDQSFTGGHAGRYLNRAGA"
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/db_xref="taxon:511"
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CCGACCATGATCGGCTCCGACGGCCTGCCGCACGACGACGACGCCCGCATCCGCGCCTGTGG
                 GAAGAAATCGCCGAGCGAGGCAAGTCCAAGTACGACGTGGTGCCCGAACTGCAGCCC 1020
                                               GATGAAGTCGCGGCCGAGCGCGAAATCCAAGTACGACGTGGTGCCCCGAGCTGCAGCCG
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                                                                       Direct Submission
Submitted (13-FEB-1995) Mamoru Wakayama, Oita University, Applied Chemistry; Dannoharu, Oita, Oita 870-11, Japan (Tel:0975-69-3311(ex.746), Fax:0975-69-7957)
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                                                                                                                                                                                 Wakayama, M., Watanabe, E., Takenaka, Y., Miyamo Sakai, K. and Moriguchi, M.
Cloning, expression, and nucleotide sequence N-acyl-D-aspartate amidohydrolase gene from A xylosoxydans subsp. xylosoxydans A-6
J. Ferment. Bloeng. 80, 311-317 (1995)
3 (bases 1 to 1497)
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                                                                                                                                        Wakayama, M.
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Sakai,K. and Moriguchi,M.
Primary structure of N-acyl-D-glutamate amidohydrolase from
Alcaligenes xylosoxydans subsp. xylosoxydans A-6
J. Biochem. 118 (1), 204-209 (1995)
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96015170
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Bacteria; Proteobacteria; !
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Alcaligenes xylosoxydans (sub_species:xylosoxydans,
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/db_xref="taxon:85698"
                                 /organism="Achromobacter
/isolate="A-6"
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GCGCGAGACGCTGCCGCTGATCGAGGCCGCCAAGGACGTCTCGCTGGACGC
                                          GGACGTGCCGGTGGTGATCTCGCACCACAAGGTCATGGGCCCAGCCCAATTTCGGCCGCTC
                                                                                                                  CGACGAAGGCGAGCACATCGTGGCCGCGCTGGAGGAAACCTTCCGCATCGGCCGCGAGCT
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/protein_id="BaA08350.1"
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ALGDENHAPGYPVIDARGLALAFGFIDSHTHDDGYLLAHPEMLPKVSQGITTVVTGNC
GISLAPLSRROIPPPLDLLGPPELFRFBTPDMIRALAETFPAAVRVIFUCVELRVA
VMDDTGRAATDAERAAMRALLDEALAGAGAFGVSTGTFYPPASAAPTDEIIDVCOPLRG
RAGAIYATHLRDEADHIVPAMEEALLIGRELDCRVVFSHKKLAGERNHGRSRETLDMI
SRAAMTQRVCLDCHYPPATSTMLIRLDRARLAETLITWSKGY PEATGRDFSEVMAELG
LDDEAAIARLAPAGAIYFLMDGADVNRLFSHPLTTVGSDGLPFDPHPPRQMGTFTNV
LRTMYREQRLLSLETALHKMTGLAAAQYGLTERGLLRQGYHADLVLFDPANVTDTATF
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1 (bases 1 to 208050)

Salanoubat, M., Genin, S., Artiguenave, F., Gouzy, J., Mangenot, S., Arlat, M., Billault, A., Brottler, P., Camus, J.C., Cattolico, L., Chandler, M., Choisne, N., Claudel-Renard, C., Cunnac, S., Demange, N., Gaspin, C., Lavie, M., Moisan, A., Robert, C., Saurin, M., Schiex, T., Siguier, P., Thebault, P., Whalen, M., Wincker, P., Levy, M., Weissenbach, J. and Boucher, C.A. Genome sequence of the plant pathogen Ralstonia solanacearum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCGGCCGAGCGCGAAATCCAAGTACGACGTGGTGCCCGAGCTGCAGCCGGCGGCGC
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Direct Submission Submitted (05-DEC Cremieux, CP5706,
                                         Boucher, C.A
                                                                                                                                                                                              Ralstonia solanacearum.
Ralstonia solanacearum
Bacteria; Proteobacteria; beta subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INRA,
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Laboratoire de Biometrie et Intelligence Artificielle INRA, BP27,
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                                                              /evidence-not_experimental complement(2462. .3139)
                                                                                                                                                                                   SFATTADDVDNLLRHMKAAAAGPSADTHATA"
complement(2462. .3139)
                                                                                                                  /note="ACUR or RS05503
predicted by FrameD"
                                                                                                                                                                                                VVAAEAIVLFDLSLAAEMGYRRKRAGHLFSKMRFLSAQIEAYLANDLWLRNARQANDM
ALRLARGLEGMHGASVLGATEANIVFCRLPSTLIENLLQAGFRFYHNRWEDNVVRFVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene name confidence: hy predicted by Codon_usage predicted by Homology predicted by FrameD"
                                                                                                                                                                                                                                               ADDCTARVEQTLSELFEREVKVFLVPTGTAÅNALCLGAMTPPWGNVYCHPSSHINNDE
JGAPEFYINGAKLVAVDGESAKIDVEKLRAATRVKVGDVHSTQPACVSLITQATEVGSL
YTLNEIEAIGQLCKDARIKLOMDGSRFANALVSLGCSPAAMTWKAGVDALSFGATKNG
                                                                                                                                                                                                                                                                                                                     translation="murdpmpttrtpalgftsdniegaspevldailaanagqaapyg
                                                                                                                                                                                                                                                                                                                                                             protein_id="CAD18267.1"
db_xref="GI:17431590"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    evidence-not_experimental
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/QRQRFKGKTVLLGPGCISLMPPGEIHDGVAEGDGAYTLKTFRLSQALLANLAQDISG
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strain="GMI1000"
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te="RS05504"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ction="small molecule metabolism;
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licted by Codon_usage
licted by Homology
icted by FrameD"
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/gene="RSp1120"
/function="miscellaneous; hypothetical/global homology"
/note="Product confidence: hypothetical
Gene name confidence: hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                 4228. .4725
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/note="RS05499"
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WGGFKAKTAPALTITHRQCGHETGLKLVCPACDEPFGPKDATVTLGASFKAERQARRD
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/note="Product confidence: hypothetical
Gene name confidence: hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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/transl_table=11
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/protein_id="CAD18270,1"
/db_xref="GI:77431593"
product="CONSERVED HYPOTHETICAL PROTEIN"
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/gene="RSp1119"
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aadntyhslcvopvivlsgdoetlkavhrralerkvphglyiedmfstghdaanravf
aehgpdsarvvgialreekkivdkitkgarmhp"
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adhhgvvlhphsdevwiahdpsaapttcvvksgnrkwwgncawcalglvhlaggsati
etrigaiddhviiriengrlldtdyvvhfpipkkhawdnviytcsvollfrdeaqvde
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/note="RS05501"
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'db_xref="GI:17431591"
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lb_xref="GI:17431592"
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'function="miscellaneous; unknown"
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TTCGACCGGCGCCTTCTACCCGCCGCCGCCGCCGCCGCCACCGAAGAGATCATCGAGGT
                                                   CGAAGTCGAAGCCATGCGCGCAGCTGCGCGAGGCGCTCGACCACGGCGCGCTGGGCCT
                                                                                  GGAAATCGCGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCATCGGCAT 593
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                                                                                                                                                       GGGCCATTCAACGCTGCGCGCGCGGTCATGCCGGACTTGCAGCGCGCCGCCGACGACGA
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AGVOIGTLYBHFPTBDALIDEIYRDEGSRLAEAARQLSEDQPPLEAVRQWLLLFYGYL
ANKQIRADVLNCMTDCSERLCTLSGEYLIETLAQLIERAKQSGAIGLAVEPLDLLSAV
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/gene="RSpl121"
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/transl_table=11
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Pred. No. 2.9e-50;
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                                                                                                                                                                                                                                                            TACCGAGCGCGCCGCCATCCATTCCGTGTACGTCAACGCCGCCGCCGGTCTGGCAAGA
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                                                                                                                                                                                                                    CAAGCAGCCGGCCGCCATCGAGGCGGTGTGGGTCAACGGCGCGCTGTCGTACCGCGA
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                                        N-acyl-D-amino acids amidohydrolase. Alcaligenes xylosoxydans (strain A-6) Achromobacter xylosoxidans
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Alcaligenes xylosoxydans DNA amidohydrolase, complete cds.
                                Bacteria; Proteobacteria;
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                       Achromobacter
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                               TCGCGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCCATCGGCATTTCGA
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813; Conservative
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Location/Qualifiers
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ADRRLDAGGRIVAPGFIDTHGHDDLMFVEKPGLEWKTSQGITSVVVGNCGISGAPAPL
PGNTAAALALIGDSPLFADMANYFGALEAQREMINVAALVGHALHLRLAAMRDPAAQPS
AKEQRAMERVLADALEAGAVGFSTGLAYQPGGVAEQAELDGLARVAAARGALHTSHIR
NEGDAVEAAVDEVLAVERRTGCATVLSSHKCMMPANMGKSAAYLANIDARRAAHTSHIR
LDIYPYPGSSTILIPERADQIDDIRITWSTPHPECGGQSLAEIAARWGCDAVVAARRL
CPAGAIYFAMDENEVRRIFGHECCMMGSDGLPNDAHPHRLMGSFTRVLGRYVREAEL
LTLEAAVAKMTALPARVFGAHEGRLAVGSDGLPNDAHPHRLMGSFTRVLGRYVREAEL
LTLEAAVAKMTALPARVFGAHEGRLAVGSDGLPNDAHPHRLMGSTDVDAPTLASAGI
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/protein_id="BAA08778.1"
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                                                                         CCGACCTGGTGGTGTTCGACCCGGCCACGGTGGCCGATACCGCCACCTTCGAACACCCTA 1375
                                                                                                  TGGACGAACCCGACGTGCAGCGCATCCTGGCGTTCGGCCCGACCATGATCGGCTCCGACG
             CCGACGTGGTCGTGTTCGACGCCGACACGGTGTGCGACCGCGCCACCTGGGACGCGCCGA
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RESULT 10 LMFLCHR34_10/c WPCOMMENT

 Sequence split into 18 fragments
 LOCUS LMFLCHR34 Accession
 AL49623

 Fragment Name
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 End

 LMFLCHR34_00
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 LMFLCHR34_01
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 LMFLCHR34_02
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 LMFLCHR34_03
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 LMFLCHR34_04
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                                  IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                  In codons is given for each CDS.

Usually the highest scoring match found by fasta o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (31.MAY-2001) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A E-mail: barrellesanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK On May 9, 2002 this sequence version replaced gi:14285271.
                                                                                                          jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most
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Unpublished
                                                                                             upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S, coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor sequencing at The Sanger Centre 1 by the BBSRC and Beowulf Genomics Details of S. coelicolor sequencing at the Sanger Centre available on the World Wide Web.
                                                                                                                                                                                                    jun/cg1-bin/frameplot.pl. CAUTION:
correct initiation codon. Where po
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Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 22251)
Redenbach, M., Kisser, H.M., Denapaite, D., Eichner, A., Cullum, J.,
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                                                                                                                                                                                                                                                                      http://www.nih.go.jp/
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the 8 Mb Streptomyces coelicolor A3(2) chromosome
Microbiol. 21 (1), 77-96 (1996)
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It may be shorter because we only sequence ns once, or longer, because we arrange for
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overlaps cosmid SCK15 and cosmid SCK13.
                                                                             1967.
                                          'gene="2SCK36.02
                                                                                              /note="Pfam match to entry PF00821 PEPCK,
Phosphoenolpyruvate carboxykinase, score 1344.70, E-value
                                                                                                                                                                                                                                                                                                               RLCGELVEKOTFRKLDPIKRRNSYYAASDPTDVARVEDRTFICSAKEEDAGPTNHWKD
PAEMRAIFTGDKGEGGLFRGSMRGRRIMYVVPFCMGPLGSPLSALGVEITDSAYVAASM
RTMRRAMGQPVLDELGDEGFFVKAVHSVGAPLEPGQADVPWPCNSTKYISHFPEDREIW
SYGSGYGGNALLGKKCYALRIASVWARDEGWLAEHMLVLKLTPPTGAPKYVAAAFPSA
CGKKNLAMLEPTISGWTVETIGDDIAWMRFGEDGRLYAINPEAGFFGVAPGTGEHTNA
NAMKTLWGNSVFTNVALTIDGDVWWEGMTEETPAHLTDWKGNDWTPESGTPAAHPNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="25CK36.02"
/gene="25CK36.02, probable phosphoenolpyruvate
carboxykinase, len: 609 aa; similar to SW:PPCK_CHLI
carboxykinase, len: 609 aa; similar to SW:PPCK_CHLI
carboxykinase [GTP] (EC 4.1.1.32) PckA, 646 aa; fasta
scores: opt: 2400 Z-score: 2689.0 bits: 507.7 E():
3.6e-142; 58.361% identity in 598 aa overlap. Contains
form match to entry PF00821 PEPCK, Phosphoenolpyruvate
carboxykinase and match to Prosite entry PS00505
                                                                                                                                                                                                                                                              ATAAAEGKVGELRRDPFAMLPFCGYNMGDYMGHWVDVAKDKDQSKLPKIYYVNWFRKD
                                                                                                                                                                                                                   LSVDKEVWREEAALVPEHLNTFGDHTPAELWDQYRALVRRLG
                                                                                                                                                                                                                                                                                           TTPAAQCPIIAPEWEDPRGVPISAILFGGRRATAVPLVTESFDWNHGVFLGANVASE
                                                                                                                                                                                                                                    AGREVWPGFGENGRVLKWIVERLEGRADGVETPIGVLPTKESLDTDGLDLADADLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'product="putative phosphoenolpyruvate carboxykinase"
'protein_id="CAC40592.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphoenolpyruvate carboxykinase (GTP) signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"putative integral membrane protein"
/protein_id="CAC40591.1"
/db_xref="GI:14285272"
/db_xref="GI:14285272"
/db_xref="GI:14285272"
/db_xref="SPTREMBL:093JL6"
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WAAVFTLPEFWRAGGVAVLVLVIVGGLLYSAGGVTYGLKRPNPSPRMFGFHEVFHSFT"
waavFTLPEFWRAGGVAVLVLVIVGGLLYSAGGVTYGLKRPNPSPRMFGFHEVFHSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MARDIAAPPVPTNHQELISWVNEIAELTQPDAVVWCDGSEAEYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref-"GI:1428527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        crans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(160. .864)

'gene="25CK36.01c"

/gene="25CK36.01c"

/note="25CK36.01c, conserved hypothetical membrane
protein, len: 234 aa; similar to SW:YA85_MYCTU

(EMBL:AL021897) Mycobacterium tuberculosis hypothetical
26.0 kDa protein RV1085c or MTV017.38c, 242 aa; fasta
scores: opt: 563 Zeore: 653.6 bits: 128.3 E(): 8.6e-29;
39.524% identity in 210 aa overlap. Contains possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         drophobic membrane spanning regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .xref="SPTREMBL:Q93JL5"
                                                                                                                                                                              2SCK36.02
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                                     밁
                                                                                           Ş
                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                            Matches
10533 CCGGGACCCAGGAGGAGTCAGGCATGGAAGAGCTGGTCATCAGGGACGCCGACGTCGTGG 10474
                                                                                                                                                                                                                                                                                                                                                                                                                                                SgS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
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RBS
                                                      CDS
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Conservative
                                                                                                                                                                                                                                                                                                                                             5801..5983
/gene="2SCK36.05"
/note="2SCK36.05, p
Contains possible h
                                                                                                                                                                        /codon_start=1
/transl_table=11
/product="putative membrane protein"
/protein_id="CAC40595.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe putative glucan synthase-1 (EC 2.4.1.34) SPBC30D10.17c, 504 aa; fasta scores: opt: 176 Z-score: 188.3 bits: 44.3 E(): 0.0071; 24.931% identity in of TR:AAK22951 (EMBL:AE005774) Caulobacter crescentus scores: opt: 146 Z-score: 160.2 bits: 38.4 E(): 0.26; 25.598 identity in 173 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note-"SC04982"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEGDLDTDRTAQGGAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mssihdfatwepilrivrashperlagpgghymgqiglggwsvp
yrrphpapgraslyddmqddetaveavqaalrahgrqsvsfmyetrydgrtalhyvds
GPAVEHGLVSPFYGTLVLVEGAVPEPHRRLPEAVPGALPAPSADPALLERTLRERLPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="2SCK36.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDQLYVADARSRPCLWQFAATDAAVTAPDAAVQGLVGSPGWIAFGDNGGGDRLALDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVGATEAEIAEAQTRLGVTLPDELKALYRVVRARWQDWRGDYAAQERVVDAVGCELLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRLGPEEWRVLLDAGAVPRSLLAAHIEVRGEHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'db_xref="SPTREMBL:Q93JL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAC40594.
/db_xref="GI:14285275"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'product-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLGTPLPGDYKRLYEIFGGAGAFDGYLQLQVPDAHDRSTDLYRHTEWLGEWARTHG
SRLWEPYPVYPAPGGLLQWASTEQADGFYWLTGDPDPDRWPVLAKEDVPDSWERFDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSGDGLEGILAAVHRITAQRMGPPVCGTAGHGTGHVCLVPPAGA
GLPGIEEAIGSREGEPLRIVTGTTTEAAGGSAGIPLRTPEGERIVEMRAWAYGDRWIG
GGTVRADDADGAVRPVYLVAERADPAAGASAPATWYDGIVAVTGWETARARAVDWPAV
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                                                                            9.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a; N-terminal region presents low similarity terminal region of TR:014362 (EMBL:297992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="2SCK36.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(3263. .4213)
/gene="2SCK36.03c"
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'protein_id="CAC40593.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="25CK36.03c"
/note="25CK36.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SAVARPELEVLVLGGREGEPRSLAPLAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 >GGHTGQVVMIGHEDSIGAGLLAESLTDMVVNGRAEWHPGRDWDRPPVVARLNVLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="PS00505 Phosphoenolpyruvate carboxykinase (GTP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (5618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 putative
                                                      Score 171.8; DB 1
Pred. No. 1.5e-10;
                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .5621)
                                                                                                                                                                                                                                                                                                                        putative membrane protein, len: 60 aa.
hydrophobic membrane spanning region*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bifunctional protein'
594.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5610)
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                                                                                                 DB 1;
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Indels 183; Gaps
                                                                                            Length 22251;
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	1051	.034TGGTGCCCGAGCTGCAGC	Оу 10
	9397	6 CCGGCACGGGCGACCCGGGGCGCTCGCCGAGTACGTCGGCCGCACGGTGCTGGAGTCGGCGC	
	1033	TACGACG	
	9457	16 AGGTGATCGGCTCCGACGGCTGCCCATGGAGTGGGAGACGATCGAGATCT	Db 95
	1003	74 AACTGAGCGGGCGGACCTGGATGAAGTCG	9
	9517	576 AGCAGATCCTGAAGCGGCTGGCGGACGACGACGACCACCACCACATGG	Db 95
	973	14 AGCAGGACCGCGTGCTGGCCGGACGGACCATCATCACCTGGTGCAAGCCCTTCCCCG	Ογ 9
	9577		Db 96
•		93 TGGCCGGCTCCACCATGCTC	Оу в
	σι	96 CCTGCTCGACGAGGCACTCGCGGGGGGGGGGGGGGGGGG	Db 96
	ο . ο	36 CGCTGATCGAGGCCGCCATGGCGCGCCAGGACGTCTCGCTGGACGCGTATCCCTACG	Оу в
	835 9697	/b TGATCTCGCACCACAAGGTCATGGGCCAGACTATTTCGGCCGCCGAGACGCCGAGACGCCGCGCGAGACGCCGACGTCGCTGCTGCTGAGGCGCGCCGACGCCCAACGTGCACAAGGGCAAAGGCGCCAACGAGGCAACAAGGGCAAAGGGCAAAGGGCAAGGCGCAACGAGGCAACAA	Db 97
	9757	16 GGCCCTGAAGGCGTACGAGGAGATGGTGGAGCTGACCCGGGAGGCGGGCTGCCCGCTGC	 vo
-	775	16 ACATCGTGGCCGCGCTGGAAGCAAACCTTCCGCATCGGCCGGGGGGGCTGGACGTGCGGTGG	Ογ 7
	715 9817	76 GCCGGGTGGTGGCGTACGGCGGCTACTACTGCCCACCACCACCGCTACGGGGGGGG	y
	78//	19. COCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCO	
	655	596 CGACCGGCCTTCTACCCGCCCGCCGCCGCCGCCACCGAAGAGATCATCGAGGTGT	36 Ad
	9937	96	v
	595	536 AAATCGCGGCCATGGGACGTGGCCGAGGAAGCCATGGCCAGCGGCGCCATCGGCATTT	
	535 9997	4/6 GCCATTCAACGCTGCGCGCGCGGCATCATGCCGGACTTGCAGCGCGCCGCCACCGACGAGGGGCII	ф 10
	10057	, (u	_
	475	416. CCGACTACCTGGACGCGTTGCGGGGCCGCCGGCCGGCCGG	
	415 10114	_	<u></u>
	101/4	,	
	358	314 CGGCCAATTGCGGCATCAGCCTGGCGCGCTGGCGCACGCCAACCC	10 84 84
	10234		_
	13	254 ACCTGCTCAGGCGTCGCGAACATGACGCCCAAGATCTCGCAGGGCGTCACCACGGTGGTCA	Qγ
	10294	.0353 ACGCCGAGGGCCTGGTCCTGTCCCCGGCTTCATCGACATGCACGCCCACAGGGACCTGG	Db 10
	253	194 ACGTGTCGGGCCTGGTGGTCGCCCCGGCTTCATCGACTCGCACACCCACGACGACAACT	Qy
-	193	152 CCATCGGCGATCTGTCGGACGCCGCGCGCACACCCG	0y 10
	151 10414	92 ACGCAGCAACACCCCGGGGCGGCGGCGGCCGACCTGGGCGTGCGCGGCGACCGCATCGCCGCGCGACCTGGGCGTGCGCGGCGACCGATCGCCGACGCGCGGCGGCGGCGGCCGATCGTTCTTACCGAGCGGCGGCGGCGGCGGACGGCCGGATCGTTCGT	Db 10
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RESULT 12
AF453501/c
                                                                                                                                                                                                                                                                                                                      REFERENCE
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KEYWORDS
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MEDLINE
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                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                              PUBMED
                                                   misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9036 CGGGCAGCTCGTTCGACGAGCCGGGGTGCTGCCTACGGGCATCCCGTACGTGCTGGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1172 GGGGCACCTTCCCGCGGGTGCTGGGGCACTATGCGCGGACCTGGGCCTGTTCCCGCTGG 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9336 CGCCGACCATCCTCCAGCACGTCGGCCACGAGGAGAACGTGCGCGCGATCATGCGGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1052 CGGCCGGCGCCATCTACTTCATGATGGACGAACCCGACGTGCAGCGCATCCTGGCGTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9396 GGCTGCGCGGCGAGAGCCCGTGGACGGTCGCCCGGCACCTGCTGCTCGCCGACCGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCTGGTCCGCGAGGGTACCGGGCCGACCTGGTGCTCTTCGACCCGGCCACGGTGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCAGCTGCAGGCCGGGTACTTCGCCGACCTGGTGGTGTTCGACCCGGCCACGGTGGCCG 1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGAGTGCGTGGCCCACCTCACCTCACGCCGGCCGGCCTGCGGCTGCCGGACCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGACGGCGGTATGGAAGATGACCGGCCTGACCGCCGCGCGCTTCGGCCTGGCCGGGCGCG
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                                                                                                                                                                                                          Direct Submission
Submitted (28-NOV-2001) Department of Chemistry,
Washington, Box 351700, Seattle, WA 98195-1700, I
                                                                                                                                                                                                                                                                                                                                                                      Yu, T.W., Bai, L., Clade, D., Hoffmann, D., Toelzer, S., Trinh, K.Q., Yu, J., Moss, S.J., Leistner, E. and Floss, H.G.
The biosynthetic gene cluster of the maytansinoid antitumor agent ansamitocin from Actinosynnemapretiosum
Proc. Natl. Acad. Sci. U.S.A. 99 (12), 7968-7973 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinosynnema pretiosum subsp. auranticum.
Actinosynnema pretiosum subsp. auranticum
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardineae; Actinosynnemataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF453501 82746 bp DNA linear BCT 18-JUN-2002 Actinosynnema pretiosum subsp. auranticum maytansinoid antitumor agent ansamitocin biosynthetic gene cluster I, partial sequence. AF453501
                                                                                                                                                                                                                                                                     2 (bases 1 to 82746)
Yu.T.-W., Bal.L., Clade,D., Hoffmann,D., Toelzer,S., Trinh,K.Q.,
Xu,J., Moss,S.J., Leistner,E. and Floss,H.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF453501.1 GI:21449342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinosynnema
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 82746)
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                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                               University of USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPELAGAASSATMGLRALLVTLLTALAGALSTGGPFAPAAVMAGAVAAVVLLSALSPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AASLTPSILLFAAYLVFIAASPFLYTAAFGLGVTGFALHLLVVVASFAVPSAFATGIIP
LLGGPAGAVRWGLGAVVVGVLGFLLLGDGPVAVTGSVALFCVGEAVCYPVVFDRSMSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAFSRVYVDTDRSAATGYAOGGIGADHLLENGSLYRHSGGGRAWTQVRVVFTEAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as hehedequreallalvarartiteatppwsaqatalvglarrvvelaaardagv
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                                                                                                                                                                 LALALELLPAPRTRLYSISSAAEEQRAEVALTVSVTGVTSGYLSRVRPGDRVAVGIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(6501. .9518)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVALTFAGQRQVFASSHELVARMCSDPSWGKAVHPALEQVRDFAGDGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(6501. .9518)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FKFSTYATWWIRQAITRALADOSRTIRLPVHMVEVVTKLÄRIERDLLHRNGREATAEE
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8.1"
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Query Match
Best Local S
Matches 758
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TGGTGATCTCGCACCACAAGGTCATGGGCCAGCCCAATTTCGGCCGCTCGCGCGAGACGC
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/protein_id="Aam54105.1"
/protein_id="Aam54105.1"
/db_xref="gl:21449373"
/translation="MPRRLAEQVVVVVGASSGIGRVTALRFAAAGARVVCAARNTRAL
/translation="MPRRLAEQVVVVVGASSGIGRVTALRFAAAGARVVCAARNTRAL
DGLVEEVRGAGGRAVAVTADIADEAAVRAVADVAVEREGRVDTWVNAAGIGVYGRVED
TPAGEFDRVMRVNYLGHVHGAKAALPALRRAGGGVLIGVASVLGLRSAPLQAPYAASK
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AGHHSDAALLGVFKVSALHULVHLAFGAAGIAAGLSKAFRGARAFLIGGGAIYAVLWL
YGVVVDEHSTANFVPLNAADNWLHLGLAVGMIGLGAALGRNAAHYRAARSDD"
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                           AGCTGGGCCAGATCGCCCTGAGCTACGAGAAGCT 1757
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                                                      CGGCCGACCCCGTCGAGCACGACACCAGCGGCCTCACCGGCTCCGAGCGCAAGGTCGCCG
                                                                                  TGACCCTGCAAGACCTGTCGCAGGCCAGCGGCATCGCGGTCTCGACCCTGTCCAAGGCCG
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                                                                                                                                           CAACCCTGGACGCAAACCGCTACATGGCCCCTCCCTCCGCTCGCAATACGGCCCCACCCG
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                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                               IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 6All Lies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             jun/cg1-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS which show significant similarity to other CDS in the database The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta on is given for the control of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1sA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
On May 9, 2002 this sequence version replaced gi.6941966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pstream initiation codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Details of S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (03-FEB-2000) Streptomyces coelicolor sequencing project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bentley, S.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6-phosphofructokinase; pta, phosphate acetyltransferase; secreted nucleosidase; sodium:dicarboxylate symporter; transcriptional regulator; trxA2, thioredoxin; two-component sensor kinase/sensor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL138978.2 GI:20520797
alpha-amylase; glgBI, 1,4-alpha-glucan branching enzyme; glycogen phosphorylase; integral membrane transport prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (inashi, H. and Hopwood, D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 28751)
Redenbach, M., Kieser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     et of ordered cosmids and a detailed
the 8 Mb Streptomyces coelicolor A3(
.Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 28751)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Research,
                                                                                                                                                                                                                                                                                                                                                                                        and overlaps with cosmids restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         et al., Gene 30:157-66(1984) as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lon is based on positional base preference in codons using ly developed Hidden Markov Model (Krogh et al., Nucleic search, 22(22):4768-4778(1994)) and the Framerlot program
/note="Nominal overlap with Streptomyces coelicolor cosmid
                                                                                                                       /db_xref="taxon:100226"
/clone="cosmid 6A11"
                                                                                                                                                                                                         /organism="Streptomyces
/strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002 this sequence version replaced gi:6941966.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 to 28751)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Beowulf Genomics
coelicolor sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kleser, H.M., Denapalte, D., Elchner, A., Cullum, J.,
                                                                                                                                                                                                                                                                                                                                              /Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detailed genetic and physical map
                                                                                                                                                                                                                                         coelicolor A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                        3D11 on
                                                                                                                                                                                                                                                                                                                                                                                                               the AseI-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ¿yme; gigp,
protein; p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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gene

CDS

gene

misc_feature

misc_feature

misc_feature

CDS

/note="SC6All.04c, possible integral membrane transport >rotein, len: 296aa; similar to many proposed transport >roteins e.g. TR:Q9X9Y6(EMBL:AL096743) putative integral

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misc_feature
/gene="SC6A11.04c"
/note="SC6A71.04c"
                                                                                                                                                   RDFLDRIVDHFWTAVERHP"
                                                                                                                                                                                            <sup>2</sup>DVARAVGLGLPAYLRMEESDDWRGTDRQSAQLADVLGLTLPDF
                                                                                                                                                                                                               /translation="mwrvrrpspgpsgsgppfnalaarrlraalnmgpehvahgirvs
/glpyvspdlviawergtalpegpeltalagvlwcspgeligrpgslrehrvarglap
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="SC6All.03c, unknown, database similarities"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="PS00433 Phosphofructokinase signature
complement(3153 .3866)
                                                                                                                                                                                                                                                                                                            'product="hypothetical protein SC6A11.03c'
'protein_id="CAB72403.1"
'db_xref="GI:6941969"
                                                                                                                                                                                                                                                                                                                                                                                           transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Pfam match to
Phosphofructokinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Pfam match to entry PF00365 PFK, Phosphoffuctokinase, score 278.20, E-value 1.6e-101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVPTAYDRVLATREGWHAVEAAHRGDEGRWTALRGTDVVMVPLAEAVTELKTVPKDRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORYMVYEVMGRHAGWIALESGMAAGAHGICLPERPFDPADLVKMVEERFSRGKKFAVV
CVAEGAHPAEGSMDYGKGAIDKFGHERFOGIGTALAFELERRLGKEAKPVILGHVORG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mrigyltääggdcpglnavirsyvhravdnygdevigfedgyagl
LDGRYRALDLNAVSGILARGGTILGSSRLERDRLREACENAGMIQNFGLDALLPIGG
EGTLTAARMLSDAGLPVVGVPKTIDNDISSTDRTFGFDTAVGVATEAMDRLKTTAESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-*SC6All.02, pfkA2, 6-phosphofructokinase, len: 341
aa; similar to many e.g. SW:059126 (PFP_AMYME)
6-phosphofructokinase from Amycolatopsis methanolica (35:
aa) fasta scores; opt: 1274, z-score: 1463.6, E(): 0,
59.1% identity in 342 aa overlap. Also similar to
from Streptomyces coelicolor (342 aa) fasta scores; opt:
1251, z-score: 1437.4, E(): 0, 56.7% identity in 342 aa
overlap. Contains two pfam matches to entry PR00365 PFK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="SC6A11.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="SC6A11.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'protein_id="6-phosphofructokinase"
'protein_id="CAB72402.1"
'db_xref="GI:60410^^-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="SWISS-PROT:Q9L1L8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphofructokinase and Prosite match to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hosphofructokinase signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nominal overlap with Streptomyces coelicolor cosmid 8F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="SC6A11.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="SC05426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="Pfam match to entry PF01515 PTA_PTB, Phosphate acetyl/butaryl transferase, score 460.50, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plement(1975. .1978)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 2804
                                                                                       .04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry
score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00365 PFK,
52.20, E-value 9.9e-19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        len: 237 aa; no significant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6-phosphofructokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              methanolica (352) 3.6, E(): 0,
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126 GGGCGTGCGCGACCGCATCGCCGATCGGCGATCTGTCGGACGCCGCCGCGCACAC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Sin
                                                                                                                                                                                                                                                                                                                                                                                                             CTCCGGGCAGGGCCACCACATCGGCCGCATCGGCCTGCGGCGGACGACGCCGAACGCAC
CACCCCGATGGGGCTGCGCCGCCGGCACATCACCAGCGAGGGCCGCACGGTCACCGC 16886
                                                                                                                                                       CCCCGTCCTCATCGACTGGCGGGCCGGTGTCGCCCGCCCCTTCTACCTGGCCACCGGCCA
                                                                                                                                                                                                            CCGGGTCGACGTGTCGGGCCTGGTGGTCGCGCCTTCATCGACTCGCACAC---CCA
                                                                                                                                                                                                                                                                                                                                                                    GCTGCTCGCCGCGCTCAACGCGGTGGACGGCTCCCTCTGCTTCGGCCGGATCGACCTCAC 16706
                                                                                                      CGACGACAACTACCTGCTCAGGCGTCGCGACATGACGCCCAAGATCTCGCAGGGCGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"SC6All.05c, possible integral membrane transport protein, len: 313 aa; similar to many proposed transport proteins e.g. TRNEW:CAB55533(EMBL:ALI17322) putative integral membrane transport protein from Streptomyces coelicolor (317 aa) fasta scores; opt: 561, z-score: 649.2, E(): 9.4e-29, 34.4% identity in 314 aa overlap. Contains Pfam match to entry pr00528 HpD_transpy Ending-protein-dependent transport systems inner membrane component, Prosite match to PS00402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Binding-protein-dependent transport systems inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane transport protein from Streptomyces coelicolor (298 aa) fasta scores: opt; 515, z-score: 609.9, E(); 1.5e-26, 33.9% identity in 295 aa overlap. Contains Pfam match to entry pr00528 BPD_transp, Binding-protein-dependent transport systems inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative integral membrane transport protein"
/protein_id="CAB72405.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inner membrane comp sig complement(4870. .5811)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sinding-protein-dependent transport systems component, score 53.20, E-value 5.7e-12" complement(4248. 4334)

'gene-"SC6A11.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLPLAWVVLSALDPHASLRVKVPDGVTLDNFDAILTPEITFTPLLNSLILCGGATLLT
VVCAVLAAYPLSRFRSRLNRPFLLTILFATSLPITAIMVPVYALFVRVNNIDTMQGTI
FFFAASQLPFAIWLMKNFMDGVPKELEEAAWTDGASSFQSLLRIVLPLMGPGVAVVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Binding-protein-dependent transport systems inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(4870. .5811)
'gene="SC6A11.05c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SC6A11.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product-"putative integral
/protein_id="CAB72404.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              component, Prosite matches to PS00402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="SC6A11.05c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'db_xref-"SPTREMBL:Q9L1L6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="SC05429"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                jene="SC6All.usc"
iote="Pfam match to entry PF00528 BPD_transp,
iote="pfam match to entry PF00528 BPD_transp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ote="PS00402 Binding-protein-dependent transport systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ranslation="MTDTVAPRPASRTSRAARRTTPAARRNRRRTAADAGLLVAAAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.18;
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                                                                                                                                                                                                                                 Submitted (31-JAN-2001) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGACCTGTCGCAGGCCAGCGGCATCGCGGTCTCGACCCTGTCCAAGGCCGAGCTGGGCC 1732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCAGACCGCGGAGGCCGGCCGGTTCGGCTCCTGGTCGAAGATCCTCGCCCCCTACGTCG 18229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTGGCGGCTGCTCATGCGCCGCTGCCCCACCCGCTCGATGACCCTGGTCGGCGACCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACGCAAACCGCTACATGGCCCCTCCCTCCGCTCGCAATACGGCCCCACCCGATATCGTGG 1612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTGGGCGTTCGGGCACATCATCGTGGACGAGGCGCAGGAGCTGTCCC-----CGATGG
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AE006004 AE005673
AE006004.1 GI:13425161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete genome sequence of Caulobacter crescentus
Proc. Natl. Acad. Sci. U.S.A. 98 (7), 4136-4141 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ely,B., DeBoy,K.I., DeBoy,K.I., Smit,J., Craven,M., Knourl,Haft,D.H., Kolonay,J.F., Smit,J., Craven,M., Knourl,Haft,D.H., Valmathevan, Tran,K., Wolf,A., Vamathevan, Salzberg,S.L., Venter,J.C., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caulobacter crescentus CB15.
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Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an,W.C., Feldbyum,T.V., Laub,M.T., Paulsen,I.T., Nelson,K.E.,
J., Heidelberg,J.F., Alley,M.R.K., Ohta,N., Maddock,J.R.,
ka,I., Nelson,W.C., Newton,A., Stephens,C., Phadke,N.D.,
DeBoy,R.T., Dodson,R.J., Durkin,A.S., Gwinn,M.L.,
D.H., Kolonay,J.F., Smit,J., Craven,M., Khouri,H., Shetty,J.,
                                                                                                                                                                                                                                                                                                                 Submission
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                                                                                                          /db_xref="taxon:190650"
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                                                                                                                                                                                                                              Qualifiers
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CB15 section
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359 of the complete
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AHIDGLIAQGKDVRVYCVGKKVTAQLAKPYAGRIVETFDLSSYRQLTLSVAQPIADVI
TREYEAGETDVVTLFYSRFKSVVQQIPTGLOLIPAVVETGEAASGPTAVYEYEPSEEA
                                                                                                                                                                                                                                                                                                                                                                   GEYDHLPEGAFYMVGPIEEAVAKAEKMAAEA"
                                                                                                                                                                                                                                                                                                                                                                                AILGMDELSEEDKLVVARARKIQRFLSQPFHVAEQFTNTPGAFVQLKDTIRSFKGIVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEVAQHLGQSTVRAIAMDATEGLVRGQÞVRDTGEÞIRVÞVGÞGTLGRIMNVIGEÞIDE
GGÞIRSDISRTIHRDAÞSFAÐGTNTAÐVLVTGIKVIDLMCÞYTKGGKIGLFGGAGVGK
TVTMQELINNIAKAYGGYSVLAGVGERTREGNDLYHEMIESNVNVDÞKANNGSTEGSR
                                                                                                                                                                                                                                                                                                          complement(3196. .4071)
                                                                                                                                                                                                                                                                                                                                                                                                          ATTVLSRDIAAQAIFPAVDPLDSTSRIMDPLVIGEEHYTVARRVQEVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1529. .3148)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note-"identified by match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="CC3447"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LREGKVTVKDGATTKVFDIQGGFADVGPEGLTILAEHAVEAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="Mylisahkgcegpsvgfnavlsscwgylayapcarqodrtrprd
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pfnvtldnpgsnknvctvtidysqapbqaqelanglhdwatwenspqlrlirndqtvg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref='
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="CC3445"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "translation="MAKLHFSLVAPERELFSGEVDMVQAPGAEGDFGVLANHAPFMTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein_id="AAK25407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product-"ATP synthase
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                                                                                                                                                                                                         'note="identified by Glimmer2; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSAYIPTNVISITDGQIFLETDLFYQGIRPAVNVGISVSRVGSSAQIKANKQVAGPIK
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protein_id="AAK25414.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="CC3451"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=
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Best Local Similarity 55.5
Matches 213; Conservative
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                                                                                                                                                                Gene cluster encoding a nystatin polyketide synthase and manipulation and utility
Patent: WO 0159126-A I 16-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1 from Patent W00159126.
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                                                                                                                                                                                                                                    Zotchev,S.B., Sekurova,O.N., Fjaervik,E., Brautaset,T., Stroem,A.R., Valla,S., Ellingsen,T.E., Sletta,H.V. and
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/organism="Streptomyces noursei"
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Best Local Similarity 43.5%;
Matches 724; Conservative
                                         20592 ACGACGAGCCCGACCTCGCCGTCCGCGGCACCGACGTGCACGCCGCCCGGCCTGGCCCGTG 20651
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Pred. No. 0.0082;
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Search completed: May 11, 2003, 03:03:11 Job time : 4976 secs

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Command line parameters:

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-O-cgn2_frame+_n2p.model -DEV-xlp
-O-cgn2_frame+_n2p.model -DEV-xlp
-O-cgn2_frame+_n2p.model -DEV-xlp
-O-cgn2_frame+_n2p.model -NEW1-0-1 -LOOPCL-0 -LOOPEXT-0
-DB-PIR_73 -OPMT-fastan -SUFFIX-FPY -MINATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-ONITS-blits -START-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MILEN-0 -MAXIEN-2000000000
-OUTFMT-bto -NORM-ext -HEAPSIZE-500 -MILEN-0 -MAXIEN-2000000000
-USER-US10009782_6CGN_1_1_46_6runat_07052003_122517_23148 -NCDU-6 -TCPU-3
-NO_MAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
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ALIGNMENTS

JC4394

R; Wakayama, M.; Katsuno, Y.; Hayashi, S.; Miyamoto, Y.; Sakai, K.; Moriguchi, M. Biosci. Biotechnol. Biochem. 59, 2115-2119, 1995
A; Title: Cloning and sequencing of a gene encoding D-aminoacylase from Alcaligenes A; Reference number: JC4394; MUID:96100942; PMID:8541651 aminoacylase (EC 3.5.1.14) - Alcaligenes xylosoxydans subsp. xylosoxydans A-6 N;Alternate names: N-acyl-D-amino acid amidohydrolase C;Species: Alcaligenes xylosoxydans subsp. xylosoxydans A-6 C;Date: 20-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 13-Sep-1998 C;Comment: This enzyme, whic resence of zinc ion or EDTA. A; Molecule type: A; Residues: 1-484 A; Accession: JC4394 Accession: ype: DNA 1-484 <WAK> which catalyzes the hydrolysis of N-acyl derivatives ofneutr

A;Gene: dan C; Geneti

C; Keywords: hydr F; 68-70/Region: C; Superfamily: aminoacylase hydrolase binding

Percent Similarity: Best Local Similarity: Query Score: Alignment No.: Match: Scores 1.64e-128 2511.00 100.00% 100.00% 76.11% Length:
Matches:
Conservative:
Mismatches: Indels: Gaps: 0000484

US-10-009-782-1 (1-1758) x JC4394 (1-484)

밁 ğ MetSerGlnSerAspSerGlnProPheAspLeuLeuLeuAlaGlyGlyThrLeuIleAsp 20

GGCAGCAACACCCCGGGGCGGCGCGCCGACCTGGGCGTGCGCGGCGACCGCATCGCCGCC 153

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DB:
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R;Wakayama, M.; Ashika, T.; Miyamoto, Y.; Yoshikawa, T.; Sonoda, J. Biochem. 118, 204-209, 1995
A;Title: Primary structure of N-acyl-D-glutamate amidohydrolase A;Reference number: JC4165; MUID:96015170; PMID:8537313
A;Accession: JC4165
A;Molecule type: DNA
A;Residues: 1-488 <WAK>
A;Residues: 1-488 <WAK>
A;Ross-references: DDBJ:D45918
A;Note: The authors translated the codon CAG for residue 132 as C;Comment: This enzyme catalyzes the hydrolysis of N-acyl derive
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C;Species: Alcaligenes xylosoxydans subsp. xylosoxydans A-6
C;Date: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 07-May-1999
C;Accession: JC4165
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Best Local Similarity:
Query Match:
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C;Superfamily: aminoa
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A; Reference number: A75001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, July 1999
A; Description: Pyrococcus abyssi genome sequence:
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Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
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625 CGCGCCACCAACGAAGAATCATCGAGGTGTGCCGGCCGCTGAGCGCGCATGGCGGCATC
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                                                       GAAGCCATGGCCAGCGGCGTTCGGCATTTCGACCGGCGCCTTCTACCCGCCGCCGCC
                                                                                  GlyMetGluAlaArgAspProThrGluGluGluLeuGlyArgMetLysGluLeuLeuAla
                                                                                                               CCGGACTTGCAGCGCGCCGCCACCGACGAGGAAATCGCGGCCATGCGGGACCTGGCCGAG
                                                                                                                                           CCGGCGGCCGTCAACGCCGCCTGTATGGTGGGCCATTCAACGCTGCGCGCCCGCGGTCATG
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hypothetical 119.5K protein (uvrA region) - Micrococcus luteus N;Alternate names: ORF 1 protein C;Species: Micrococcus luteus, Micrococcus lysodeikticus C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_chang
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                                                                                                                                                          GGCATCCATTCCGTGTACGTCAACGGCGCGCGGTCTGGCAAGAGCAGGCGTTCACCGGC 1449
                                                                                        AspAlaGlyGlyValValIleArgArgThrSer
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TyrSerLysThrTrpGluLeuIleGluLeuAlaMetValValAlaLysTyrGlyGlyIle
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#text_change 04-Feb-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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R;Shlota, S.; Nakayama, H.
MOI. Gen. Genet. 217, 332-340, 1989
A;Title: Micrococcus luteus homolog of the Escherichia coli uvra gene: identifica A;Reference number: S04781; MUID:89364717; PMID:2549377
A;Accession: JQ0405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-1106 <SHI>
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{\tt aArgGlyProArgProGlnGlyArgValArgGlyProValGlnGlyProValHisAlaGl}
                                                                                             ACGAGGAAATCGCGGCCATGCG------GGACCTGGCCGAGGA-----AGCCATGG
                                                                                                                                  aAlaAspArgGlyProAlaArgGlyAlaAlaArgAlaHisProLeuProGlyAlaArgAl 237
                                                                                                                                                                           TGCGCGCCGCGTCATGCCGGACTTGCAGCGCGCCGCCAC------
                                                                                                                                                                                                              YThrCysArgGlyAlaAlaLeuProAlaValArgArgAlaGlyGluProAlaAspProAl
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	493	473 aProLeuHisHisGlyLeuArgGlyArgHisProLeuArgAspAlaGlnAlaArgG	밁
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	790	<pre>// CCTTCCCCATCGCCCCCAGCTGGACCTGGACCGGGGGGGGAGCTGATCTCGCACCACA // CCTTCCCCATCGCCCCCCGCGCGCGCGCGGGGGGGGGG</pre>	B 15
	305	295 -HisProProAlaProHisArgLeuGlyG) B
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ent Scores: 5.19e-11 No.: 5.19e-11 338.50 t Similarity: 35.59% ocal Similarity: 28.50% Match: 10.26%	protein [imported] crobacterium ammonie n-2000 #sequence_rev 745.34 46, 1996 ing and characterize umber: 222923; MUID: 745.34 liminary; translated pe: DNA 1590 <str> ences: EMBL:X79027; 1 source: ATCC 15354</str>	31 TGCCGCCCCCTC 1542 73 SerAlaProLeu 576				118 GACCTGGTGGTGGTTCGACCCGGCCACGGTG	ω ω	CGCGACCTG ArgAspArgThrArgGly	50 GAGCGCCCGCATCCGCGGCCTGTGGGGCACCTTCCCGCGGGTG : : : 57	8 TT	66 TACTTCATGATGGACGAACCCGACGTGCAG 	18 AAATCCAAGTACGACGTGGTGCCCGAGCTGCAGCCGGCC 	8 GACCTGGA 7 AspProAs
Length: 529 Matches: 181 Conservative: 45 Mismatches: 198 Indels: 211 Gaps: 30	bacterium ammoniaphilu 21-Jan-2000 #text_char 21-Kessler, C. f the Mami restriction 50; PMID:8654988 GB/EMBL/DDBJ		 ValArgG	AACGGCGCGCCGGTCTGGCAAGAGCAGGCGTTCACCGGCCAGCATGCCGGCCG	CACCCTACCGAGCGCGCCGCCGCCATTCCGTGTACGTC	GCCGATA ArgLeuGluAlaProG	CTGACCGCCGCGCGCTTCGGCCTGGCCGGGCGGGCAGGTGCAGGCCGGGTACTTCGCC 	CGCGACCTGGGCCTGTTCCCGCTGGAGACGGCGGTATGGAAGATGACCGGC 	CTGGGG AsnLeuIle	CGGCCCGACCATGATCGGCTCCGACGGCCTGCCGCAC	pProser	ලි :	T
	um (fragment) ige 21-Jul-2000 i-modification system		572	GGTGCTC 1470 ::: gLeu 567 GGCGGCG 1530	RGTACGTC 1410 nrileval 548	CCGCCACCTTCGAA 1368 :::::: lnValAlaTyrAsp, 528	CCGGGTACTICGCC 1317 roGlyTyrArgAla 508	rGACCGGC 1257 ::: lnSerArg 488	CACTATGCG 1206 ::: HistrpThr 468	GAC 1149 eCysAsp 456	CGCATCCTGGCG 1107 ::: ::: PhealaMetLeuSer 436	GCGCCCATC 1065 ::: lyArgGlyMetLeu 416	AGCGCGGC 1017 rgGluGly 396

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protein her lip-Mar-1997 lon: \$27923 lon: \$27924 lon: \$27925 lon:	AlaArgi	HisLeu GATATC	YLeuLeu AACCCTG	AGCAGGCGTTCACC- : nAlaSerAla-ThrL	TACCGAG Glyarga	GGTGGTGTTCGACCCGGC- ArgGlyProArgGlnGlyG	CGGGCAG ArgLeuH	GACG	ATGCG uArgHisF	GCACGAC Alaala <i>t</i>	GTTCGGG	TGCAGCCGGCCGCCCC	CGACCTO	;AlaAlai
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4 4 n 19-Mar- n 19-Mar- 1, S.; Ba ugust 199 tion of R	CGGAAAATGACCCTGCAAGACCTGTCGCAGGCC 	HisleuAspvalThrThrTrpArgAlaAspAlaSerIleSerArgArgThr CCGATATCGTGGGCAAGGAAGTGATGGGGGCGCGCGCGCG	1	AGCAGGCGTTCACCGGCCAGCATGCCGGCCGCGTGCTCGCACGCACGGCCG 	CTACCGAGCGCGCCGGCATCCATTCCGTGTACGTCAACGGCGCGCCGGCCTGTGCAAG 	-GGTGGTGTTCGACCCGGCCACGGTGGCCGATACCGCCACCTTCGAACACC 	GCGGGCAGCTGCAGGCCGGGTACTTCGCCGACCT	GACGGCGGTATGGAAGATGACCGGCCTGACCGCCGCGCTCGGCCTGGCCGGGC ::: pHisProGlnGlyLeuGluGlyAlaAlaGlySerArgArgHisProHisArgLeuArgAl	ATGCGCGCGACCTGGGCCTGTTCCCGCTGGA	CGCACGAGCGAGCGCCCGCATCCGCGGCCTGTGGGGCACCTTCCCGGGGGTGCTGGGGCACT	CGTTCGGCCCGACCATGATCGGCTCCGA	TGCAGCCGGCCGGCGCCATCTACTTCATGATGGACGAACCCGACGTGCAGCGCATCCTGG 	GCGACCTGGATGAAGTCGCGGCCGAGCGGGCAAATCCAAGTACGACGTGGTGCCCCGAG ArgargGlyargAlaAspGlyCysargA	gAlaAlaHisArgGluAlaLeuHisLeuArgLeuGlnAr
Barr virus 9-Mar-1997 #text 5.; Barrell, B.; st 1990 n of Raj1 Epste1	AGGCC	Alaseriles		GCCGCG	STCAACG lavalLe	GCCGATA	GACCT rgProAr	GCCGCGC rgArgH1	lyProG1	ACCTTCC laargPr	rgProAr	.CGAACCCGACGTGCAGCGCATCCTGG ArgAlaArgArgAlaGlyGlyGlyGl	TCCAAG	lnArg-
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	Db 201AlaspProValGly	1	84 ArgLes 279 GCCCA 103 GlyHii 339 GCC 123 ThrPrc	 C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal hom Alignment Scores: Pred. No.: Score: S
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THIM IN THE PROCESS OF THE PROCESS O	PI PI S	AlaAlaAspProAlaA CCTTCGAACACCCTA-	ס-ש מ-ט	 287 ThrArgLeuGlnProAlaThrProArgArgSerGlyAlaAlaAspProAlaAspProVal 306 849 CGCCATGCGCGCAGGACGTCTCGCTGGA

	214 rogluArgGlySerGlyProAlaAspProProAlaAlaAlaArgLeuProProGluArgG 234 447 GGCGGCCGTCAACGCCGCCTGTATGGTGGGCCCATTCAACGCTGCGCGGCGGCGTCATGCC 506 :	196 AlaAlaProGlyProGlyGlyGlyAlaAlaValProSerGlyAlaThrProHisp 214 423 CCTGGACGCGTTGCGGGCCA	303 CACGGTGGTCACGGGCAATTGCGGCATCAGCCTGGCGCCGCTGGCGCACGCCAACCCGCC 362		183 CACCCGGGTCGACGTGTCGGGCCTGGTGGTCGCCCCGGCTTCATCGACTCGCACACCCA 242 169 Hispro 170	123 CCTGGGCGTGCGGCGACCGCATCGGCCATCGGCGACGCCGCCGCCGCCGCCGCA 182	69GCTCGCGGGGGGCACCCTCATCGACGGCAGCAGCACACCCCGGGGGCGGCGCGCCGA 122 133 LeuGlySerArgGlyProArgProHisProAlaPheGlnValGlnTrpSerAlaArgAsn 152	39 CCAATCCGAGTCCCAGCCTTCGACCTGCT	s-10-009-782-1 (1-1758) x QQBE3 (1-660)	29.04% Mismatche 9.75% Indels: 1 Gaps:	milarity: 31.83% Conservative:	es:	PMID:6087149 on trepeats (residues 149-2	ature 310, 207-211, 1984 **Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome. **Reference number: 103704: https://doi.org/10.10070677	Type: DNA 1-660 <ban> Banklor a T. Diccio M. D. D. Diccio M. Diccio M. D. Diccio M. D. Diccio M. D. Diccio M. Diccio</ban>	Filte: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus reference number: A93065; MUID:85035713; PMID:6092825	P.L.; Farrell, P.J.; Barrell, B.G.	cies: h		b 646 iGlyHisProAlaAlaProArgAlaPro 655		Db 626 gThrargLeuGlnProAlaThrProArgArgSerGlvAlaAlaAspDroAlaAspDroX
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1476 CACGGCCGCCTGAGCCCGGCGCCAGCCCTTACAATCCGGCGTGAACGGGGGGGG	516 ArgArgProProGlyCysProArgSerAlaArgAsnProGlyCysProArgThrTrpA 535 1416 CGCGCCGGTCTGGCAAGAGCAGGCGTTCACCGGCCAGCATGCCGGCCG	496 GlnArgCysProAlaGlyProProProThrArgSerGlyAlaAlaAlaGlnArgThrH18 515 1362 CTTCGAACACCCTACCGAGCGCGCCGCCGGCATCCATTCCGTGTACGTCAACGG 1415	1263 CGCCGCGCGTTCGGCCCGGGCCGGGCGGG	GTTCC ValPr	1182 CCCGCGGGTGCTGGGGCACTATGCGCGCGGACCTGGGGCCT	1143 GCACGACGAGCGCCC	1083 ACCCGACGTGCAGCGCATCCTGGCGTTCGGCCCGACGATGATCGGCCTCCGACGGCCTGCC 1142	1023 CAAGTACGACGTGGTGCCCGAGCTGCAGCCGGCGGCGCCCATCTACATGATGATGACGA 1082	362 ArgLeuProGlnAspLeuAlaAlaAlaGlnArgCysProAlaGlyProPro 378	342 GlySerGlyProAlaAspProProAlaAlaAlaArgLeuProProGluArgGlnGluPro 361 963 GCCCTTCCCCGAACTGAGCGGGGGGGGCGATGATGTAGTCGCGGGCGAGCGCGGCAAATC 1022		322 AlaProGlyProGlyGlyGlyAlaAlaValProSerGlyAlaThrProHisProGluArg 341	318GlyThrProAla 321	798 GGGCCAGCCCAATTTCGGCCGCTCGCGCGAGACGCTGCCGCTGATCGAGGCCGCCATGGC 857	738 AACCTTCCGCATCGGCGCGCGAGCTGGAGGTGCTGGTGATCTCGCACCACAAGGTCAT 797	86	2/1 YsProArgSerAlaArg-AsnProGlyCysProArgThrTrpArg 285	627 CGCCACCGAAGAGATCATCGAGGTGTGCCGGCCGCTGAGCGCCATGGCGCATCTA	259	567	507 GGACTTGCAGCGCCGCCACCGACGAGGAAATCGCGGCCATGCCGGGACCTGGCCGAGGA 566	

Db 127 GlyGluGlySeralaGlyLeuGlySerArgGlyProArgProHisProAlaPheGlnVal 146 Qy 1597	red. No. 2002 e. 2002	Oy 1536 CCCCCTCCCAACCCTGGACGCAAACCGCTACATGGCCC
Qy 868 CGTCCTGGCGCG	Db 383 GlyAlaAlaValProSerGlyAlaThrPro	Qy 1534GGCACGCCGGTTCACGCCGGATTGTAAGGGCTG Db 207 ProSerGlyAlaThrProHisproGluArg
CGTCCTGGCGGG	GlyAlaAlaAlaYalProSerGlyAlaThrProHisProGluArgGTTQCAGGTAGGCTGCAGGT 1088 GlyAlaAlaAlaYalaAlaAlaYalaAlaYalaAlaYalaAlaYalaAlaYalaAlaYalaAlaYalaAlaYalaAlaYalaAlaYalaAlaYalaAlaYalaAlaYalaAlaYalaAlaYalaAlaYalaAlaYalaAlaYalaYa	

GCACCCTCATCGACGGCAGCAACACCCCGGGGCGGCGCGCGCGCGACCTGGGCGTGCGCG 136 ::: ::: ::: ::: SerProThrProSerSerProAlaSerProArgSerProThrValArgCysArg 54	CCATGTCCCAATCCGATTCCCAGCCCTTCGACCTGCTCCCCGGGGC 79 ::: ProSerProSerProThrSerProThrProProSerProSerThrGluSer 36		rercent Similarity: 33.24% Conservative: 37 Best Local Similarity: 28.01% Mismatches: 195 uery Match: 9.31% Indeals: 277 B: 2 Gaps: 45	2.68e-09 Length: 307.00 Matches:	A;Note: the authors designated this protein as endo-glucanase	A HUA>	submitted to the EMBL Data Library, September 1990 A;Description: Nucleotide sequence of a cellulase gene complex from Ruminococcus flavefa A;Reference number: S21323	-	endoglucanase - Ruminococcus flavefaciens	656ProArgThrTrpArg 660	ACAGATCGCCGATGGCGG 149			TCATGTCGCGACGCCTGAGCAGGTAGTTGTCGTGCGAG	337 CCAGGCTGATGCCGCAATTGCCCGTGACCACGTGGTGACGCCCTGCGAGATCTTGGGCG 278	GluArgGlnGluProArgLeuProGlnAspLeuAlaAlaAlaGlnArgCysProAlaGly	394 AGCCGCCTTCGTCCAGCAGGTCCAGGGGGGCGGGCGGGTTGGCGTGCGCCAGCGCG 338		73 ProGlyProGlyGlyGlyAlaAlaValProSerGlyAlaThrProHisProGluArgGly. 592	ProAlaAlaProGlyAlaProGlyThrProAlaAla	CGATITCCTCGTCGGTGGCGGCGCGCGCGCGCGCGCGCGTTG 48	543 -GlyH1sProProProGlyAla	טי נ
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923 GCGTGCTGGCCGGACGCACCATCATCACCTGGTGCAAGCCCTTCCCCGAACTGAGCG 982 323 pGlyAlaGlyArg	-GI AGG					238 nArgGlyArgArgH1sArgLeuValAspArgArgValArgProArgGluGlnProValPr 258	::: pGlyProSerAspGlyArgSerP	:::		536 AAATCGCGGCCATGCGGGACCTGGCCGAGGAGGCATGGCCATGGGCATTT 595 :::	-ProHisAspAla	476 GCCATTCAACGCTGCGCCGCCGCCGTCATGCCGGACTTGCCAGCGCCGCCGCCACCGACGAGG 535	419 ACTACCTGGACGCGTTGCGGGCCACCGCCGGCGGCCGTCAACGCCGCCTGTATGGTGG 475		131 uLeuValGlyGlnLeuValH18ProGlnSerGlyLeuValProValValArgGlyValPr 151 359 CGCCGCCCCCTGGACCTGCTGGACGAGGGCGCTTTACCGTTTACGAGGCGCTTTACGCG 418	Ċ	111 aCysHisGlyProSerValHisArgAlaAspTrpHisGlnProArgArgAlaAlaLeuGl 131	: ±:-	ATTGCGG	25/ TGCTCAGGCGTCGCGACATGACGCCCAAGATCTCGCAGGGCGTCACCACGGTGg 310			137 GCGACCGCATCGCCGCCATCGGCGATCTGTCGGACGCCGCGCCGCGCACACCCCGGGTCGACG 196

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A;Title: Mucl. a mucin-like protein that is regulated by Mss1
A;Reference number: JC6123; MUID:96323337; PMID:8710886
A;Accession: JC6123
A;Status. JC6123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: SGD:MUC1; STA2; MAL5; DEX;
A;Cross-references: MIPS:YIR019c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEBS Lett. 239, 179-184, 1988
A;Title: Similar short elements in the 5' regions of the A;Reference number: S27281; MUID:89031230; PMID:3141213
A;Accession: S27281
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J. Bacteriol. 169, 2142-2149, 1987
A;Title: Gene fusion is a possible mechanism underlying A;Reference number: A91831; MUID:87194600; PMID:3106330
A;Accession: A26877
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A; Residues: 1-1367 <LAM>
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A; Residues: 762-1331 <YA2>
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A; Residues: 1-242 < YAM>
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A; Residues: 1-31 < PAR>
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PID: 9172526

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1367 139 72 266 68

--ProValProThrPro

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436

	1390	1331 TCGACCCGGCCACGGTGGCCGATACCGCCACCTTCGAACACCCTACCGAGCGCGCCGCCG 1
	759	740 ProserserThrThrGluserserSerAlaProValThrSerSerThrThrGluser 7
	1330	1271 GCTTCGGCCTGGGCGGGGGGGGGGGTGCTGCAGGCCGGGGTACTTCGCCGAGCTGGTGTT
	739	720 aProValProThrProSerSerSerThrThrGluSerSerSerAlaProValProThr
	1270	1211 ACCTGGGCCTGTTCCCGCTGGAGACGGCGGTATGGAAGATGACCGGCCTGACCGCCGCGC
	1210 720	701 Gluser-SerAlaProValProThrProSerSerThrThrGluserSerSerAl 720
	700	1151 AGCGCCCGCATCCGCGCTCTGTGCGGGCATCTTTTCCCCCCCTGTTTTCCCCCCCTGTTTTTTTT
	1150	1097 GCATCCTGGCGTTCGGCCCGACCATGATCGGCTCCGACGGCCTGCCGCACGACG
	680	661 ThrGluSerSerSerAlaProValProThrProSerSerSerThrThrGluSerSerSerSer
	1096	1037 TGCCCGAGCTGCAGCCGGCCGGCGCGCTGCTACTTCATGATGGACGAACCCGACGTGCAGC
	660	641 ProSerSerShrThrGluSerSerAlaProValProThrProSerSerSerThr
	1036	977 TGAGCGGGCGCGACCTGGATGAAGTCGCGGCCGAGCGGCGAAATCCAAGTACGACGTGG
	54 0	621 SerSerSerAlaProValThrSerSerThrThrGluSerSerSerAlaProValProThr
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	940	y 881 CGTATCCCTACGTGGCCGGCTCCACCATGCTCAAGCAGGACCGCGTGCTGCTGGCCGGAC
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	0 0	Y 821 CGCGCGAGACGCTGCCGCTGATCGAGGCGCTGATCGCCCCCCCC
	n 0	
	D (761 TGGACGTGCCGGTGGTGATCTCGCACCACAAGGTCATGGGCCAAGCCCAATTTCGGCCCGT
	760	54.5
	U	y 701 GCGACGAAGGCGACACATATCCTCCCCCCCCCCCCCCCC
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		Y 641 AGATCATCGAGGTGTGCCGGCCGCTGAGCGCATGCATCCCCATCTATCT
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	514	7 F
	580	3y 521 CCGCCACCGACGAAGATCGCGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCG
	510	
	520	29 461 CCGCCTGTATGGTGGGCCATTCAACGCTGCGCGCGGTCATGCCGGACTTGCAGCGCC
	490	Db 471 AlaprovalThrSerSerThrThrGluSerSerSerAlaprovalProThrProSerSerSer
	460	DY 413 TCGCCGACTACCTGGACGCGTTGCGGGCCACGCCGGCGGCCGTCAACC
	470	bb 457 ProvalProThrProSerSerSerThrThrGluSerSerSerSe
•	מול ב	QY 353 CCAACCCGCCCCCCCCTGGACCTGCTGGACGAAGGCGGCTCTTACCGTTTTCGACCCC
•	355	43
	, 1	Qy 293 AGGGGGTCACCACGGTGGTCACGGGCAATTGCGGCATCAGCCTGGCGCATCACCGTGGCACCACGTGGTGGCACGGTGGTGGGTG

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Best Local Similarity:
Query Match:
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(;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Nov-1999
C;Accession: T02345
R;Ricke, D.O.; Bruce, D.; Mundt, M.; Doggett, N.; Munk, C.; Saunders, E.; Robinson, re, J.; White, S.; Ueng, S.; Tatum, O.; Campbell, C.; Fawcett, J.; Deaven, L. submitted to the EMBL Data Library, March 1998
A;Description: Sequencing of human chromosome 16p13.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 16
A; Introns: 1610/2;
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A; Residues: 1-1791 <RIC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Note: KIAA0324
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                            1480 CCGTGCGTGCGAGCACGCGGCCGGCATGCTGGCCGGTGAACGCCTGCTCTTGCCAGACCG 1421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1511 CCGGCGTGAACGGGGGGGGGGGGCGCCCCCCCCAACCCTGGACGCAAACCGGCTACATGG 1570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1451 AGCATGCCGGCGCGCGCGCACGCACGCCCGGCCCGAGCCCCAGCCCCTTACAAT 1510
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                                                                         SerProGluHisProProLysSerArg---
                                                                                                                         SerGlySerSerSerLysGlyArgGlyProSerProGluGlySerSerSerThrGluSer 689
                                                                                                                                                       AGGGAGGGCCATGTAGCGGTTTGCGTCCAGGGTTGGGAGGGGGCGCCACG------ 1529
                                                                                                                                                                                       -----GluProLysAlaProAlaPro----ArgAlaLeuProArgArgSerArg
                                                                                                                                                                                                                     GCAGGCGCGCCCATCACTTCCTTGCCCACGATATCGGGTGGGGCCGTATTGCGAGCGG
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                                                                                                                                                                                                                                                                               CCCCTCCCT 1579
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---ThrAlaArgArgGlySerArgSerSerPro----- 708
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296.00
35.61%
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Matches:
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	728	GGTGCGAGATCACCACCGGCACGTCCAGCTCGCGGCCGATGCGGAAGGTTTCCTCCAGCG	Qy
	872	nGluSerSerArgThrSerSerArgArgArgArgGly	밁
	788	GAGCGGCCGAAATTGGGCTGGCCCATGACCTTGT	Qγ
,	U	rgSerArgSerArgValThrArgArgArgArgClyGlySerGlyTyrHisSerArgSer	D.
	ω	GCCACGTAGGGATACGCGTCCAGCGAGACGTCCTGGCGCGCCATGGCGGCCTCGATCA	Qγ
	836	Ser	망
	9	GGTGCGTCCGGCCAGCAGCACGCGGTCCTGCTTGAGCATGGTGGAGC	δð
	835	SerArgArgArgGlnArg	밁
	959	GCGACTTCATCCAGGTCGCGCCCCGCTCAGTTCGGGGGAAGGGCTTGC	δ
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	803	784 ArgThrLysThrThrSerArgArgGlyArgSerProSerProLysProArgGlyLeuGln	ర్జ
	1079	CGCCAGGATGCGCTGCACGTCGGGTTCGT	Q.
	783	766 GluProAlaGluLysSerArgSerSerArgArgArgArgSerAlaSerSerPro	D
	1133	1192 GCACCCGCGGGAAGGTGCCCCACAGGCGCGGGATGCGGGCGCTCGTCGTGCGGCAGGCCGT	νQ
	765	erProSerVal	D
	1193	AGTGCCC	φ
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	1241	1300 GCAGCTGCCCGCGCCCGGCCAGGCCGAAGCCGCGGCGGCGAGGCCGGTCATCTTCCATA	Qy
	N	(D	ઠ
	1301	1360 TGGCGGTATCGGCCACCGTGGCCGGGTCGAACACCCACCAGGTCGGCGAAGTACCCCGGCCT	Qγ
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	1361	1420 GCGCCCGTTGACGTACACGGAATGGATGCCGGCGCGCGCG	φ.

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2	Db dd	US-10	Alignme Pred. N Score: Percent Best Lo Query M DB:	Oy O	Q.
118 00000000000000000000000000000000000	58 TTGACCTGCTGCTGCGGGGGGGGGCACCCTCATCGACGGCAGCAACACCCCGGGGGGGG	10-009-782-	lignment Scores: 1.34e-08 Length: 611 core: 294.00 Matches: 153 ercent Similarity: 36.48% Conservative: 79 est Local Similarity: 24.06% Mismatches: 216 uery Match: 8.91% Indels: 190 B: 2 Gaps: 25	986 ThFATGGT-1919. 986 ThFATGGT-1920 AGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	421 AGTCGGCGAAGCGCTCGAAACGGTAAGAGCCGCCTTCGTC

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118 GCCGACCTGGGCGTGCGCGGCGACCGCATCGCC-----GCCATCGGCGATCTGTCGGAC 171

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965	TGCAAGCC	Y
379	359 nGluLeuLeuAlaAspArgSerTyrArgArgSerPheArgArgGluPheAspArgIleLy	5
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μ.	GCTGGACGTGCCGGTGGTGATCTCGCACCACAAGGTCATGGGCCAGCCCAATTTCG	Ϋ́
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<u>1</u> 5	33 ValLeuGlyAlaLeuArgAspAsnGln	8
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390	SOC	8 8
112	96 H1sGlyValThrThrValLeuLeuGlyAsnCysSerLeuSerThrValT	8
ω.	GCGTCACCACGGTGGTCACGGGCAATTGCGGCATCAGCCTGGCGCGCTGG	Ϋ́
95	76 ValHisThrHisTyrAspAlaGluValLeuLeuAspProGly	문
, ,	2 TOGCACACGACGACGACGACTACCTCCTCCTCAGCCTCAGCCTCAGCATAACAACAACTACTCAGCATTACCTCAGCATTACCTTCAGCATTACCTTCAGCATTACATT	8
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55	36 ArgThrLeuGlyIleArgAspGlyValValAlaThrValAlaAlaGlyAlaLeuAspGlu	₽

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RESULT A43932 mucli N;Alter N;Alter C;Spec; C;Acces R;Gum . Biol A;Title A;Refer A;Resic A;Refer	О У	D 04	D Qy	Ф	Ş	р _О у	Db Qy	D Q	윰 1	S B	. Qy	B 7	g B	Qy	망	νQ	₽.
RESULT 14 A43932 N;Alternate C;Species: H C;Date: 10-M C;Date: 10-M C;Date: 10-M C;Date: 10-M R;Gum Jr., J J Biol. Che A;Ritle: Mol A;Reference A;Accession: A;Coss-refe A;Gum Jr., J Biol. Che A;Ritle: The A;Ritle: The A;Ritle: The A;Rocession: A;Rocess	1487 598	1453 584			1373	1313 524	1253 505	4 2 2	465	1196	1139	429	.416	1026	398	966	379
cursor, intestinal - human (fragments) names: mucin SMUC-41 Homo sapiens (man) dar-1993 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999 i.R.; Hicks, J.W.; Toribara, N.W.; Siddiki, B.; Kim, Y.S. na. 269, 2440-2446, 1994 lecular cloning of human intestinal mucin (MUC2) cDNA. Identificati number: A49963; MUID:94132002; PMID:8300571 i.A49963 i.A45106 ii.A45106 ii.A45106 ii.A45106 iii.A45106 i		33	94 TCATTCCGTGTACGTCAACGGCGCGCGGCGGTCTGGCAAGAGCAGGCGTTCACCGGCCAG- 1452 	luGluAlaValProTyrTyrGlyGlyLeuArgArgMetValAsnArgAsnAspAlaThrV	3 CTACCGAGCGCGCCGCCGCA	13 TCGCCGACCTGGTGGTGTTCGACCCGGCCACGGTGGCCGATACCGCCACCTTCGAACACCC 1372	53 CCGGCCTGACCGCCGCGCGCTTCGGCCTGGCCGGGCGGGC	UI UI	. G	5 oAsnGlnLeuAsnLysLeuAiaAlaGluProSerValHisMetGlyPheSerAspAlaGl	9	29 nGlyGluArgAsnValArgTrpThrThrileValAlaAsnHisArgPr 445	9 61	GTACGACGTGGTGCCCGAGCTGCAGCCGGCCGGCGATCTACTTCATG	98 oAspLysSerLeuIleGlyLysSerPheGlyAlaIleAlaAspGluArgGly 415	66 CTTCCCCGAACTGAGCGGGCGCGACCTGGATGAAGTCGAGCCGAGCGAAATCCAA 10	sLeuGlyProSerLeuTrpH1sArqAspPheH1sAspAlaValIleValGluCv
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Pred. No.:
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:Cross-references: GDB:120203; OMIM:158370

:Map position: 11p15.5-11p15.5

:Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology;

:Keywords: 91ycoprotein; intestine; tandem repeat

:2766-2834/Domain: von Willebrand factor type C repeat homology <VWC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Experimental source: bronchus; Xu, G.; Huan, L.; Khatri, I.; Sajjan, U.S.; McCool, D.; Wang, D.; Jones, C.; Forstne: iochem. Biophys. Res. Commun. 183, 821-828, 1992; Title: Human intestinal mucin-like protein (MIP) is homologous with rat MIP in the C; Reference number: PQ0328; MUID:92198477; PMID:1550588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: protein
Residues: 2328-2342,'K',2344-2354 <XUG1>
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Residues: 1343-1350,'L',1352-1411,'S',1413-1448,'P',1450-1503,'T',1505-1915 <TOR>
Residues: 1343-1350,'L',1352-1411,'S',1413-1448,'P',1450-1503,'T',1505-1915 <TOR>
GROWN Teferences: GB:M74027; NID:9188863; PIDN:AAA59875.1; PID:9188864
Note: sequence inconsistent with the nucleotide translation
Note: sequence extracted from NCBI backbone (NCBI:55749, NCBIP:55750)
Gum, JR.; Byrd, J.C.; Hicks, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S.
Biol. Chem. 264, 6480-6487, 1989
LiTitle: Molecular cloning of human intestinal mucin cDNAs. Sequence analysis and evaluation and the sequence analysis and the sequence ana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: GB:M86523
Experimental source: small intestine
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Residues: 2328-2468 <XUG>
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;Title: Human bronchus and intestine express the same mucin gene.;Reference number: A61257; MUID:91086481; PMID:1985113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: PQ0329
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A;Note: sequence extracted from NCBI backbone (NCBIP:116706)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: mRNA
Residues: 'T',1925-1948,'TTS',1952-1954 <JAN>
                                                                                 1383 LysIleArgValAsnCysCysTrpProMetAspLysCysIleThrThrProSerProPro 1402
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Toribara, N.W.; Gum Jr., J.R.; Culhane, P.J.; Lagace, R.E.; Hicks, J.W.; Petersen, Clin. Invest. 88, 1005-1013, 1991
Title: MUC-2 human small intestinal mucin gene structure. Repeated arrays and polym Reference number: A43932; MUID:91358717; PMID:1885763
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Residues: 2037-3020 <GU3>
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        20 AAGGAGAGATTTCCATGTCCCAATCCGATT-----
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289.50
32.92%
25.70%
8.78%
Mismatches:
Indels:
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Matches:
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GCAAGCCCTTCCCCGAACTGAGCGGGCGGGCCGACCTGGATGAAGTCGCGGCCGAGCGGGCACCGGGCCGACCCGACCCGACCCGACCCGACCCGACCCGACCCGACCGCCACCCACCCACCCACCCACCCCACCCCACCCCACCCCACCCC	CGCACCACAAGGTCATGGGCCAAGCCCAATTTCGGCCGCTCGCCGCAGAGGCCTGCCGCTGA ::: ::: TCGAGGCCGCCATGGCCGCGCGAGGACGCTTGCCT	CGGCCATGCGGCCGCCGCCGACGACGACGACGACGACGACGACGACG	CLACGESTREGTCAGGGCAATTGCGGCATCAGCCTGGCGCCGCTGGCGACGCCAACCCCCC	The Thir Proser proproprofibrith that he the Leupro
erPro-	GCTCA	GGGAG H H MetTh ACCCG H H ThrTh ThrTh ThrTh	GTCAC	CTACTA
ACTGA hrIle CGAAC hrThr hrThr CGGCTT	TGGGC	CTGGCC Thread	GGGCAA	erProj
AGCGGG	CAGCCC ::: cThrPr CAGGAC Th CACCGC ThrTh	STORIGO COGREGATE CO	GGACG	ProProProThrThrThrThrThrLeuPro
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GGCGCGACCTGGATGAAGTCGCGGCCGAGCGGCA	GCTGGC	TGCAGE THATH TGGCC2 TGGCCC CCACCC PhrPrc CCACCA PhrPrc CCACCA PhrPrc	AGCCTG GCTCT GCGTCT HILLI Prose	IT The The The Leupro
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TCCTGG	CGCGAC	GACGAC GACC GACGAC GACC GACGAC GACC GACGAC GACC GACGAC GACC GA	GCTGG	LeuPro
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GCCGAGCGCCA : : : -ProThrThrThr CCGGCCGGCGCCA : : : : rThrProSerPro 3CGTTCGGCCCGA : : ProThrThrThr GCCTGTGGGGCA	CTGCCGCTGA	ThrTh ThrTh TTTCG TGTGCA AGCACA THE TGTGCA T	GGGGCACGCCAACCCCC	CGCCGC
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118 84 84 63 63 67 77	1543 841 1548 898 898 1562 1562	1500 601 1511 661 1523 1523 721 1532	361 1463 421 1473 481 1489	1418 181 1434 241 1448 301 1455

711 ArgProGlyGluGlyAlaArgAl	Db	Db 406 AlaArgGlyArgArgAlaValValAlaArgGlnValHisLeuGlyLeuLeuAlaAla 425
844 CGATCAGCGGCAGCGTCTCGCGC	Qγ	1684 GCGACAGGT
691 ValArgHisArgArgLeuProLe	Дb	391
856CCATC	Qy	QY 1744 TCAGGGCGATCTGGCCCAGCTCGGCCTTGGACAGGGTCGAGACCGCGATGCCGCTGGCCT 1685
671 ArgValArgArgArgGlyArgA	ф	US-10-009-782-1 (1-1758) x JQ0405 (1-1106)
898 CGGCCACGTAGGGATACGCGTC	Qy	2 Gaps:
665H1sA	Db	cal Similarity: 32.81% cal Similarity: 27.84%
958 ACCAGGTGATGATGGTGCGTCC	Qy	287.50 Length:
::: 646 ProHisArgArgAlgAlaArgA	ф	Scores:
994 CCAGGTCGCGCCCGCTCAGTTC	δδ	this protein overlaps uvrA gene
 -626 ProAlaGlyGlnProProProH	<u>р</u>	Cross-references: EMBL:X15867
	φ	
titi CGAACGCCAGGATGCGCTGCAC 612 ArgArgProI-myArgProArgA	문 5	A; Accession: J00405
) E	MO1. Gen. Genet. 217, 332-340, 1989
	y Qy	C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 04-Feb-2000 C;Accession: JQ0405
573 GlyValProAlaGlyArgArgF	Д	names: ORF 1 prote
1225 GGAACAGGCCCAGGTCGCGCGC	ν	etical 119.5K protein (mrs. socios)
562 GlyProGlyAlaGlnGly	Ф	SULT 1
1285 CGGCCAGGCCGAAGCGCGCGGC	Qy	:::
2 AlaArgGlyHis	Db	1745 ThrThrLeuProProThrThrThr
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473 AlaProLeuHisHisGlyLeu	ф	
1513 CGGATTGTAAGGGCTGGCGCC	Qy	1671 ThrThrThrProproProPhrThrThrProproproProThrThrThrProproproPhrThrThrProproproPhrThrThrProproproproThrThrThrProproproproPhrThrThrProproproproPhrThrThrThrPropropropropropropropropropropropropropr
453 ArgProAlaArgGlnGlyLeu	В	1355CCGCCACCTTCGAACACCCTTCGAACACCCCCCCCCC
1558TTGCGTCCAGGGTTG	Qy	Db 1652 proProThrehambases 1354
440 Hisproval	ДD	
1606 TATCGGGTGGGGCCGTATTGC	Qy	238 CGGTATGGAAGAT
426 ArgAla	망	1634
1666 TCATTITCCGGGCCTTGCGCT	γQ	Qy 1178 CCTTCCCGCGGGGTGCTGGGGCACTATGCGGCGCGGGGCCTGGTTCCCGGTGGAGACGG 1237

	GinGly 986	985	밁
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11	FICGAAGGGCTGGGAATCGGATTGGGACATGGAAATCTCTCCTTCCGCGATCA	70	Ωy
974		958	ర్జ
71	GAGGGTGCCGCCCCGCGA	124	δ.
957		942	뭥
125	GATCGCCGATGGCGGCGATGCGGTCGCCGCGCACGCCCA	163	Ş
941	SerGlyLeuArgProSerGlyProAlaArgHisHisAlaLeuGlyArgArgGlyProAla	922	B
164	AGCCGGGCGACCACCAGGCCCGACACGTCGACCCGGGTGTGCGCGGCGGCGTCCGACA	223	ρy
921		907	밁
224	TGGGCGTCATGTCGCGACGCCTGAGCAGGTAGTTGTCGTCGTGGGTGTGCGAGTCGATGA	283	δÃ
907	uHisArgArgGlyProArgHisAlaAspArgGlyGlyArgGlyLeuLeuGlnArgVa	888	밁
284	GCGGCGCAGGCTGATGCCGCAATTGCCCGTGACCACCGTGGTGACGCCCTGCGAGATCT	343	Ş
888	gGlyValProArgGlyProValGlnProGlyAspAlaArgGlyHisLeuGlnGlyGlnGl	868	В
344	AGCCGCCTTCGTCCAGCAGGTCCAGGGGGGCGGGCGGGTTGGCGTGCGCCA	394	8
868		848	밁
395	CGGCCGCCGGCGTGGCCAACGCGTCCAGGTAGTCGGCGAAGCGCTCGAAACGGTAAG	454	Qy
•		835	당
455	GCAAGTCCGGCATGACCGCGGCGCGCGCAGCGTTGAATGGCCCACCATACAGGCGGCGTTGA	514	Ş,
835	<pre>pProGlnAlaLeuArgGlyAspProArgGlyGluGlyProGlyLeuProAlaGlyProVa</pre>	815	밁
₩.		552	δõ
\vdash	uProHisArgAlaHisAlaThrLeuGlnProArgHisLeuHisGlyArgValArgArgAs	795	밁
553		586	δ
795	::ArgGlyGlyThrArgAlaProGlyGlnGlyGlyProArgGlyProGl	780	ర్జ
587	CTTCGGTGGTGGCGGGGGGGGGGGGGGGGGAAAGGCGCGGTCGAAATGCCGA	640	δĀ
779	ProGlyGlnProAlaGlnArgArgGlnAlaArgAla-ArgProAlaProVal	763	g
641	TGCCGCCATGCGCCTCAGCGGCGCACACCTCGATGATCT	682	δō
762	ValArgLeuArgGlnValHisAlaAspGlnArgAspProLeuGlnGly	747	밁
683	CGGCCACGATGTGCTCGCCTTCGTCGCGCGCATGTGGGTGG	727	Ş
4	l ArgLeuGlyProGlyProAlaArgGlyProHisGlyArgAspGlyArg	731	日
728		784	Ω

Pleted: May 11, 2003, 12:12:51 84.5 secs

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-MODEL-frame+_n2p.model -DEV-x1p
-Q-/cgn2_1/USPTO_spool/US1009782/runat_07052003_122519_23229/app_query.fasta_1.1927
-Q-/cgn2_1/USPTO_spool/US1009782/runat_07052003_122519_23229/app_query.fasta_1.1927
-DB=Pending_Patents_AA_New -QFMT-fastan -SUFFIX=rapn -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS_bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pcc -NORM=ext -HEAPSIZE-500 -MINLEN=0 -MAXLEN=200000000
-USER-US10009782_eCGN_1 1_42_exunat_07052003_122519_23229 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEY_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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-MODEL-frame+_n2p.model
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                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                     Score
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                                                                                                                                                                                                                                                                                                     Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
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US-10-366-683-17231

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APPLI	FILIN	APPLI	FILIN	APPLI	FILIN	APPLI	FILIN	APPLI	FILIN	APPLI	FILIN	APPLI	FILIN	APPLI	NT FIL	CURRENT APPLICATION NUMBER:	FILE REFERENCE: ELITRA. 034A	OF IN	CANT:	CANT:	CANT:	CANT:	CANT:	CANT:	CANT:	CANT:	CANT:	CANT	CANT:		ч'		_
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					2000-09-09	NUMBER: 60/230,347	2000-09-06	NUMBER: 60/230,335	2000-05-26	NUMBER: 60/207,727	2000-05-23	NUMBER: 60/206,848	2000-03-21	NUMBER: 60/191.078	2003-0	MBER:	.034A	entifi		•	Roberi	r†	o B	el :	udith	1	Robe	ervl	Carlos	5	LETON	1	
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US-10-282-122A-50211
658 CGGCCGGTGAGCGCGATGGGGGGGATCTACGCCACCCACATGCGCGACGAAGGCGAGCAC 717
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR ETLING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
SOFTWARE: Patentin version 3.1
TENGIH: 475
                               211 TieLeuGluAiaMetAspGluAlaTyrArgValGlyArgHisAlaArgValProValVal
                                                                                               191 GluProLeuAlaAsnAlaGlyAlaValTyrThrThrHisMetArgThrGluPheAspAla 210
                                                                                                                                                              171 SerGlyLeuAlaTyrGlySerAlaPheAlaAlaProThrGluGluValMetAlaLeuAla 190
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A-60254 Applica RMATION: Wang, Liang Zamudio, Ch Haselbeck, Ohlsen, Ka, Zyskind, Ji Zyskind, Ka Zysk	TTACA	ThrGL	ACCGG	Alani	GCCGC	:: Valle	GTGGI	: : :		IIIII	TGCGC	: : : OASnA:	GCACG	 	Acccc	rGluG	CAAGI	apProH	AGCCCI	erSer	CCACC	engin	TCGAG	erHis
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Best Local Similarity:
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
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                     164 IlealaGlyMetArgValGlnLeuArgAspAlaLeuArgGlnGlyAlaLeuGlyLeuSer
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DR FILLING DATE: 2000-12-22
DR APPLICATION NUMBER: 60/267,636
DR FILLING DATE: 2001-02-09
DR APPLICATION NUMBER: 60/269,308
DR FILLING DATE: 2001-02-16
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FILING DATE: 2000-11-27
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APPLICATION NUMBER: 60/230,335
FILING DATE: 2000-09-06
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FILING DATE: 2000-05-23
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Sequence 10819, Application U
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSH
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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 10819
LENGTH: 530
TYPE: PRT
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                                           GluTyrGlyGlyTyrTyrCysProH18H1sArgSerTyrGlyAlaGlyAlaLeuGlnAla
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US-10-156-761-11333

Sequence 11333, Application US/10156761 GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT:

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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
VUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11333
TYPE: PRT
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Best Local Similarity:
Query Match:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Streptomyces avermitilis
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                    218 AlaGluLeuLeuAlaLeuAlaArgAlaValGlyGluHisGluGly------
                                                         198 GlnSerSerThrHisSerAspGlyAspGlyGlnProValAlaSerArgHisAlaArgPro 217
                                                                                                                  544 GCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCATCGGCATTTCGACC--- 600
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CAGCATGCCGGCCGCGTGCTC ::: AlaValProGlyLysValLeu	GGCATCCATTCCGTGTACGTCAACGGCGCGCCGGTCTGGCAAGAGCAGCGGTTCACCGGC	ACCGCCACCTTCGAACACCCT	CTGCAGGCCGGGTACTTCGCCGACCTGGTGGTGTTCGACCCGGCCACGGTGGCC ::::: :::	GUGGTATGAAGANGACCGGCCTGACCGCCGCGCGCTTCGGCCTGGCCGGCGGGCAG 	Thr	A	ACCATGATCGGCTCCGACGGCCTGCCGCACGACGACGACGCCCGCATCCGCGCCCTGTGGGGC	ProAspSer	GluIleCys	GAGCTGCAC	GlyArgvalvalAsnAspIleAlaAlaGluArgGlyGlnAspProPheHisCysLeuval	GGGCGCGAC	AlaAsnPheGlyArgTyTValIleGlyAs	ValArgAl	GTGGCCGGCTCCACCATGCTCAAGCAGGAC	TrpGlyGl	1	::: LeuTh	GCCATGGC	GluArgAl	cccrc	AsnValLe	GGC	AspAlaG1	AGC		
GCCGCGTG ::: yLysval	CCGTGTAC :: ::: laValTrp	TCGAACAC euValH1s	GGTACTTO ::: PheHis	AAGATGACO ::: MetLeuTh	ArgPheLeuGlyAspCysLeuArgGlyArgLysLeuValProLeuGluGln	GlySerAspAlaGlyAlaHisLeuAspArgMetCysGlyAlaProTyrThr	GCTCCGA	TOAspSerTrpAlaLeuArgAla	AlaAlaAs	AGCTGCAGCCGGCGCGCCCATCTACTTCATGATG	.valAsnAs	CTGGATG	GGACGCAC GlyArgTy	GluLeuL	TCCACCA:	pGlyGluValLeuGlyLeuProValProGluArgIleAlaArgLeuArgAs		LeuThrProMetAsnMetSerLeuGlyThrPheCysAlaLeuAsnLeuIleProG	GCGCCAGG	::: ::: LuargalaargLysalaGlyGlyargValValalaLeuThrMetPro	-CGCTCGCGCGAG-	nValLeuThrIleAs		laGluileAspLeuPheValGluMetSerAlaAlaAlaGlyArgProLeuAspTrp	CGTGCCGG	ThrGlnIleGluAlaIleValAlaGlvCvsLeuAspGlnPho	ATGCGCGACGAAGGCGAGCACATCGTGGCCGCGCGCTGGAGGAAACCTTCCGCATCGGCCGC
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	GTCTGGCA :: AlaIleAr	spSerProAr	TTCGACCO	CGCTTCG	GACCTGG GlyArgL	::: 1AspArgM	CAGCGCC	pArgHisL	lLeuTrpf	GATG	gGlyGln.	CGGCAAAT	CTGGTGC! ::: TYrSer!	rLysGlu		.uArgIle		::: PheCys		alAlaLeu		luArgVal		erAlaAla	ACAAGGTO	lvCvsLei	CGCTGGAG
	GCCGGTCTGGCAAGAGCAGGCGTTCACCG L	ACC	cggccacg roalaarg	GCCTGGCC lyLeuArg	GCCTGTTC ysLeuVal	etCysGly	CGCATCC	ysaspva	roMetPr		spProPh	CCAAGTA	-ACCTGGTGCAAGCCCTTCCCCGAACTGAGC ::: PThrTyrSerThrAlaAsnGluGlvLouThr	AlaGlyVa	-	AlaargLe		AlaLeuAs		::: ::: ::: :::	ACGCTGC	Š.		: AlaGlyA	Aregeco	AspGlab	GAAACCT
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RESULT 5

QY 513 GCAGCGCGCCGCCGACGAGGAAATCGCGGGCCATGCGGGGAACCTGGCCGAGGAAGCCAT 572	791	165 GTCGGACGC	US-10-009-782-1 (1-1758) x US-10-366-683-17231 (1-2294) Qy 9 CTTGATCGCGGAAGGAGATTTCCATGTCCCAATCCGATTCCCAGCCCTTCGACCTGCT 68	Alignment Scores: Pred. No.: 8.45e-09 Length: 2294 Score: 455.00 Matches: 238 Percent Similarity: 34.51% Conservative: 36. Conservative: 36. Query Match: 13.79% Indels: 281 Gaps: 46	APPLICANT: NUBERIELD, MARC J. APPLICANT: Nolling, Jork APPLICANT: Nolling, Jork APPLICANT: Deloughery, Craig APPLICANT: Descriptor, Craig APPLICANT: Descriptor, Craig APPLICANT: Descriptor, Craig APPLICANT: Descriptor, Craig FIITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE REFERENCE: PATH03-04 FILE REFERENCE: PATH03-04 FILE REFERENCE: PATH03-04 CURRENT APPLICATION NUMBER: US/10/366,683 CURRENT APPLICATION NUMBER: 09/252,991 PRIOR APPLICATION NUMBER: 09/252,991 PRIOR FILING DATE: 1999-02-18 PRIOR FILING PSECO ID NOS: 33142 SEQ ID NO 17231 CREANISM: PSeudomonas aeruginosa US-10-566-683-17331	Cavana 1/21, Application US/10366683
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AAGA - yas	LYA1	36	ACCT	laGl	CA	GCGT laG1	lnPı	GA	::	TCC1	laa	TSA	AGC	Alac	GCTG	H1SA	CACC	ArgG 	ProA		G1yc	GGTO	Ala	GGA	Ser	GCG		AGA	laT	CGG
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US-10-419-128-17231, Application US/10419128; Sequence 17231, Application US/10419128; GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS; FILE REFERENCE: 107196.136
           Percent Similarity:
Best Local Similarity:
                                                                 Alignment Scores:
Pred. No.:
                                                                                                                  ; ORGANISM: Pseudomonas aeruginosa
US-10-419-128-17231
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                                                                     AlaProGlyGlnLeuArgThrValGlyLeuGlyAsp-----GlnProLeuGlyAla
                                                                                                          GCCGGTGGTGATCTCGCACCACAAGGTCATGGGCCCAGCCCAATTTCGGCCGCCTCGCGCGA
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993	SULT 8 -10-419-128-26129 Sequence 26129, Application US/10419128 Sequence 26129, Application US/10419128 GENERAL INFORMATION: APPLICANT: Marc J Rubenfield et al. TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/10/419,128 CURRENT FILING DATE: 2003-04-21 PRIOR APPLICATION NUMBER: US/09/252,991 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/074,190 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 26129 LENGTH: 885 TYPE: PRI ORGANISM: Pseudomonas aeruginosa 10-419-128-26129	666 Pro 666	1740 CCT 1742	665	1722 CGAGCTGGGCCAGATCGC 1739	 AlaHisLeuGln	GCAAGACCTGTCGGAGGCGAGCGGGATCGCGGTCTCGATCGTCTCTATAGACCTGTCGGAGGCGAGCGGGATCGCGGATCGGGATCGTCTGTCGAGGGGATGGGATGGGGATGGGGATGGGGATGGGGATGGGGATGGGATGGGGATGGGATGGGATGGGATGGGATGAT	GAGCGCAAGGCCCGGAAAATGACCCT	_	. 60					530 LeuArgThrSerArgAlaLysAlaLeuProArgArgAlgAlaValProHisglySer 549	GCAGGGTTCACCGGCCACCATTCCCCCCCCCCCCCCCCC	THE PROPERTY OF THE PROPERTY O	509	1359CACCTTCGAACACCC 1373	470 ProValValAlaAlaProAlaGlyArgArgArgThrGluProGlyLeuArgProAspPro 489	1347 1358	450 ProGluArgProAlaProGlyThrGlyAlaCysGlnProAlaMetAlaAlaGlyThrArg 469	1320 CCTGGTGGTGTTCGACCCGGCCACGGT 1346

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US-10-419-128-19446

Sequence 19446, Application US/1041912

GENERAL INFORMATION:

APPLICANT: MACC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND CURRENT APPLICATION NUMBER: US/10/419,128

CURRENT APPLICATION NUMBER: US/09/252,991

PRIOR APPLICATION NUMBER: US/09/252,991

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190
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Best Local Similarity:
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SEQ ID NO 19446
LENGTH: 937
                              342 LeuLeuGlyArgLeuGlnArgArgProGlnGlyGlnValGlnLeuHisArgAlaGlyGly 361
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Query Match:
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US-10-366-683-30843
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PRIOR FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/366,683 CURRENT FILING DATE: 2003-02-13
                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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APPLICANT: Nolling, Jork
APPLICANT: Deloughery, Craig
APPLICANT: Bush, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID ITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS ILE REFERENCE: PATHO3-04
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86 TCATCGACGGCAGCAACACCCCGGGGCGGCGGCGCGACCTGGGCGTGCGCGGGGACCGCA 145
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Deloughery, Craig
Bush, David
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	н" н	-ArgArgArgAlaAlaAlaProGlyLysArgArgSer	1699 GCGGTCTCCAACGCCCAAGGCCGAGCTGGGCCAGATCG 1738	631 -AlaproGlyAlaAlaThrGlyAlaProThrThrGlyAlaAlaArgPro 646	1639 CGCGCCGAGCGCAAGGCCCGGAAAATGACCCTGCAAGACCTTGTTGTAGGCCAAGGCCAAGGCCCATTGTAGGCCAAGGCCCAAGGCCCAAGGCCCAAGGCCCAAGGCCCAAGGCCTGCAAGGCCTTGTAGGCCAAGGACCAAGGACCAAGGACAAGGCCAAGGCAAGGCCAAGGCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCAAGAAG	620 gCysSerProArgArgProThrProArgSer	1588 AATACGGCCCCACCCACCACCATATTCCTCCCCACCACCACCACCAC		582 eAlaAlaProAlaGlyProThrProAlaArgProProAlaAlaAlaThrGlyAr 60	1468 CTCGCACGCACGGCCGCGTGAGCCCGGCGCGCGAGCCCTTACAATCCGGCGTGAACGGCGCG 15	562 aArgProArgAlaProArgArgProGlyArgSerProAlaThrAlaProAlan = 1	1414 GGCGCGCCGGTCTGGCAAGAGCAGGCGTTCACCGCCACGCCCATGCCCCAAGAGCAGG	542 SProAlaAlaGlyArgArgProSetProAlaProAlaProAlaProAlaProAlaCaracGTGTAAC	1354 ACCGCCACCTTCGBACACCGTTTCGBACACGTTTCGBACACGTTTCGBACACGTTTCGBACACGTTTCGBACACGTTTTCGBACACGTTTCGGTTTTCGGTTTCGGTTTCGGTTTTCGGTTTTCGGTTTTCGGTTTTCGGTTTCGGTTTCGGTTTCGGTTTTCGGTTTTCGGTTTTCGGTTTTCGGTTTTCGGTTTTCGGTTTTCGGTTTTCGGTTTTCGGTTTTCGGTTTTTCGGTTTTCGGTTTTCGGTTTTTCGGTTTTTCGGTTTTCGGTTTTTCGGTTTTTCGGTTTTTT	524 OALAHISATERENGSARALI CHILIKUT III III III III III III	1294 CAGCTGCAGGCCGCGTTACTTTCAGGCCGCTAGGCGCGCGC	504 PARTATEMENT 1 1 1 1 1 1 1 1 1	12681252 yang and Adama AlaCysTyrProProProAlaProGl	484 GAlaArgThrGlvIleArgArgThrAleArgThrAleArgThrAleArgThrGlvIleArgArgThrAleA	12591259	464 YAlaGlyProAlaSerThrGlyArgSerArgArgArgArgArgArgArgArgArgArgArgArgArg	1215GGGCCTGTTCCCGCTGGAGAGAGGCGCGGTATGCAGGAGAGAGGGGGGGG	444 eAlaGlySerAlaProGlySerGlyThrAlaProArgCvsu(CT	1172 GGGGCACCTTCCCGGGGGGGGGGGGGGGGACTATGCGGGGGACTATGCGGGGGACTATGCGGGGGACTATGCGGGGGACTATGCGGGGGACTATGCGGGGGACTATGCGGGGGACTATGCGGGACTATGCGGGACTATGCGGACTATGCGGGACTATGCGGGACTATGCGGACTATGCGGACTATGCGGACTATGCGGACTATGCGGACTATGCGGACTATGCGGACTATGCGACTATGCGGACTATGCGACTATGCGACTATGCGACTATGCGACTATGCGACTATGCGACTATGCACTATATGCACTATGCACTATGCACTATGCACTATGCACTATGCACTATGCACTATATGCACTATGCACTATATGCACTATATGCACTATGCACTATGCACTATATGCACTATATGCACTATATGCACTATATGCACTATATGCACTATATGCACTATATGCACTATATGCACTATATGCACTATATGCACTATATGCACTATATGCACTATATGCACTATATGCACTATATGCACTATATGCACTATATGCACTATATATGCACTATATGCACTATATATGCACTATATGCACTATATATGCACTATATATGCACTATATATA	425 aAlaAspHisProAlaAlaTrpValSerAlaAlaArgArgThrSerSerSerSerSerSerSerSerSerSerSerSerSerS	1112 GCCCGACCATGATCGGCTCCGACGGCTTGCTGCTGCTACGACGGGGGGGG	405 9AlaThrProAlaSerAspAlaArgargargargarals	1058 GCGCCATCTACTTCATGATGATGATGATGATGATGATGATGATGATGATGATGA	386 UATGARGE	1013 GCGGCAAATTCAACTACCACTACTACTACTACTACTACTACTAC	953 CCTGGTGCAAGCCCTTCCCCCGAACTGAGCGGGCGGGCCGACCTGGATGAAGTCGCGGCCGAGC	353 ProAlaGlyProArgProSerCysThrAlaValAlaAlaTrpAlaProAlaArg	905 CCATGCTCAAGCAGGACCGCGTGCTGCTGGCCGGACGCACCATCATCA	

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	571	CCACCGACGAGGAAATCGCGGCCATGCGGGACCTGGCCGAGGAAG	
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	523	CCTGTATGGTGGGCCATTCAACGCTGCGCGCGCGGTCATGCCGGACTTGCAG	
	133		
	463	AGCGCTTC	Qy 407
	114	SerSerAlaProAlaProAlaAsnCysCysCysLeuPheProAlaGlyProSerProAl	Db 95
	4	CGCACGCCAACCCGCCCGCCCCCTGGACCTGCTGGACGAAGGCGGC	Оу 347
	9 (Db 75
•	۵ 4	GCATCAGCCTGGCGC	Оу 326
	74	4	Db 6
		6 GTCGCGACATGACGCCCAAGATCTCGCAGGGCGTCACCACGGTGGTCACGGGCAATTG	Оу 26
	တ ၂	u	Db 5
	265	TGGTGGTCGCCCCGGCTTCATCG	Оу 206
		40 ArgValProAlaCysArgArgValProIleArgCysAlaAsnAla	Db 4
	N .	TCGCCGCCATCGGCGATCTGTCGGACGCCGCCG	Оу 146
	39	24 TrpSerThrThrArgProProAlaAspArgSerGlyAlaThrAla	Db 2
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		13.11% Indels: 6 Gaps:	
		432.50 Matches: Similarity: 33.51% Conservati al Similarity: 27.52% Mismatches	Score: Percent Best Loc
		of Scores: 6.37e-08 Length:	Alignment Pred. No.
	•	ORGANISM: Pseudomonas aeruginosa 0-419-128-30843	; ORGAN US-10-419
		NO 30843 H: 663	SEQ II
		APPLICATION FILING DATE	; PRIOR ; PRIOR
)R PEPLICATION NUMBER: US 60/074,788 REFILING DATE: 1998-02-18	; PRIOR
		RENT FILING DATE: 09/10/419,148 REPLICATION NUMBER: US/09/252,991	CURRENT
PSEUDOMONAS	TO	INVENTION: NUCLEIC ACID AND A INVENTION: AERUGINOSA FOR DISTREBUCE: 107196.136	; TITLE ; FILE ; CURREN
		PLICANT: Marc J. Rubenfield et al	; APPL

1294 CAGCTGCAGGCCGGGTACTTCGCCGACCTGGTGGTGTTCGACCCGGCCACGGTGGCCGAT 1353	ζy
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371 GlyGlyTyrAlaAlaAlaProArg-AsnSerCysSerAlaGlyArgIa 786	ДD
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353 ProAlaGlyProArgProSerCysThrAlaValAlaAlaTrpAlaProAlaArg 370	дд
CCGGACGCACCATCATCA	20
336 ProTrpSerAlaValAlaLysThrSerProTrpProArgTrpProGlyMet 352	рb
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251 ThrAlaArgArgSerProSerThrAsnGlyArgProAlaAlaCysProThrThrThrPro 270	ДD
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 211 TrpLysProCysAlaCysAlaLysAlaValGlySerAlaArgSerProAlaAsnAlaTro 23	탕
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بر در	Pred. No.: 6.64e-08 Fred. No.: 822 Score: 9431.50 Percent Similarity: 31.108 Best Local Similarity: 13.088 Conservative: 34 Conservati	PRIOR APPLICATION UNMBER: 09/252,991 PRIOR FILING DATE: 1999-02-18 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 21920 LENGTH: 822 TYPE: PRT ORGANISM: Pseudomonas aeruginosa US-10-366-683-21920	A A A A A A A A A A A A A A A A A A A	001.0-6	1588 1639 631	1468 582 1528 600	Db 524 oAlaH19ArgProSerAlaSerAlaThrGlyTrpProGlyProAlaLeuAlaCy 542 Qy 1354 ACGGCCACCTTCGAACACCCTACCGAGCGCGCGCGGCATCCATTCCGTGTACGTCAAC 1413
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Sequence 21920, Application US/10419128
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SECTIFIE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/10/419,128
CURRENT FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: US/09/252,991
PRIOR FILING DATE: 1999-02-18
                                                                                                                                                                 RESULT 14
US-10-419-128-21920
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US-10-419-128-21920
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21920
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TYPE: PRT
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                GATCATCGAGGTGTGCCGGCGCTGAGCGCGCATGGCGCATCTACGCCACCACGTGCG
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                                                                                      CGCCATCGGCATTCGACCGGCGCCTTCTACCCGCCCGCCGCCGCGCGCACCACCGAAGA
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	234 GCACACCACGACGACAACTACTGCTCAGGCGTCGCGACATGACGCCCAA	114 GGGGGCGACCTGGGGGGGGGGGACCGCATCGGCGATCGGCGATCTGTCGGACGC :::	3-10-009-782-1 (1-1758) x US-10-366-683-32204 (1-651) 54 GCCCTTCGACCTGCTGCTGCGGGGGGCACCCTCATCGACGGCAGCAACACCCCGGGGGCG [lignment Scores: red. No.: 430.50 Matches: 208 srcent Similarity: 34.57% Conservative: 35 set Local Similarity: 29.59% Mismatches: 247 13.05% Mismatches: 247 13.05% Findels: 38 s-10-009-782-1 (1-1758) x US-10-366-683-32204 (1-651) 54 GCCCTTCGACCTGCTGCTGCTCGCGGGCGGCACCCTCATCGACGGCAGCAACACCCCGGGGCG 11 GCGCCGGACCTGGGCGTGCGCGGGCGACCGCATCGGCGGATCTGTCGACGGCGGCG 11 GCGCGCGACCCTGGGGCGTGCGCGGCGACCGCATCGGCCATCGGCGATCTGTCGACGC 11 GCGCGCGACACCCCGGGTCGACCGCATCGGCCATCGGCGATCTGTCGACGC 11 GCGCGCGACACCCCGGGTCGACGCGACCGCATCGGCGATCTGTCGACGCC 11 GCGCGCGACACCCCGGGTCGACGGCGACCCTGGTGGTCGGCGACCCTCATCGGCGACCCTCATCGGCGACGCTCATCGACTGCGCCTCATCGACTGCTGTTCGACTGC 11 GCGCGCGACACCCCGGGTCGACACTGGTGTCGGCCCCGGCTTCATCGACTC 11 GCGCGCGCACACCCCGGGTCGACACTGCTGGTCGGCCCCGGCTTCATCGACTC 11 GCGCGCGCACACCCCGGGTCGACACTACCTGCT	1566 CATGGCCCCTCCGCTCGCANTROGGCCCCACCGANTAGGLA

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_	222	SerAlaGluAlaGlyGlyArgGlyProArgGlyPheLeuGlnProHisArgHisArgHis 241
	690 242	CACCCACATGCGCGA 731 :::
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	262	ValArgGlyGlyArgLeuProHisArgAlaSerGlyGluAspAla 276
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	834	GCCGCTGATCGAGGCCGTCGAGGACGT
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	954	GAACTGAGCGGGCGCGACCTGGATGAA
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	429	roProArgGlyAsnProCysLeuGlnCvsArgGlnProGlyPr

Search completed: May 11, 2003, 12:28:05 Job time : 108 secs

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; SEQ ID NO 9018
; LENGTH: 492
; TYPE: PRT
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APPLICANT: Gary Brand
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: PUBLICACID FOR DIAGNOSTICS A
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A.
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                           ORGANISM: Klebsiella
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Best Local Similarity:
Query Match:
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LENGTH: 558
TYPE: PRT
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APPLICANT: Mitsuhashi, Kazuya APPLICANT: Yamamoto, Hiroaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/770,517C CURRENT FILING DATE: 2001-01-26 PRIOR APPLICATION NUMBER: JP 2000-019080 PRIOR FILING DATE: 2000-01-27 PRIOR APPLICATION NUMBER: JP 2000-150578 PRIOR FILING DATE: 2000-05-22 NUMBER OF SEQ ID NOS: 27
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APPLICANT: Tokuyama, Shinji
TITLE OF INVENTION: D-AMINOACYLASE AND GENE ENCODING
FILE REFERENCE: 06501-072001
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124 AspGluGluCysArgThrThrLeuLysGlyValGlyMetPheGluTrpGlnThrIleGly
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                                                            AsnValAspGlnLeuArgAlaIleArgGluGlnIleAlaGlyTrpAsnGlyAsnProThr 12:
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                           GGGCGCGGGCAGCTGCAGCCGGGTACTTCGCCGACCTGGTGGTGGTGTTCGACCCGGCCACG
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                                                                                                 LeuProSerMetIleAlaHisLeuThrSerArgProAlaLysArgLeuSerValTyrPro 483
                                                                                                                                                     CTGTGGGGCACCTTCCCGCGGGTGCTGGGGCACTATGCGCGGGCCTGGGGCCTGTTCCCG 122
                                                                                                                                                                                                                                                                                                             HisArgValHisMetAlaGlySerAspGlyIleLeuHisGlyGlnThrLeuHisProArg
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Best Local Similarity:
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TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONA
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
ILENGTH: 2294
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
18-09-252-0814-17231
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                                                          -----ArgArgValProAlaAla
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100)81 ProGlyGlnProArgProGlyGlyGlnGlyArgLeuAlaGlyLeuProArgProAlaGln 110	1081	B
097	GATGGACGAACCCGACGTGCAGCG 1	1074	Ą
080	LeuArgLeuValValH1sArgArgSerGlyAlaAlaGlyH1sArgArgProLeuTyrH1s 1	1061	В
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040	l ArgAspHisArgProAlaArgPheGlyGlnAspHisArgAlaAspGluLeuArgProGly 1	1021	Ď
983	CGAACTGAGCGG	972	Ã
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971	4 CGTGCTGCTGGCCGGACGCACCATCATCACCTGGTGCAAGCCCTTCCC 9	924	Ą
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9	7 CGGCTCCACCATGCTCAAGCAGGACCG	897	γQ
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896	7 GCTGATCGAGGCCGCCATGGCGCGCCAGGACGTCTCGCTGGACGCGTATCCCTACGTGGC	837	Ş
960	 AspArgProAlaValProGlyLeuAspArgLeuProArgAlaAlaHisArgAlaGlyPro	941	ğ
836	8 GACGCTGCC	821	Ϋ́
940	AlaProGlyGlnLeuArgThrValGlyLeuGlyAspGlnProLeuGlyAla	924	Дb
827	8 GCCGGTGGTGATCTCGCACCACAAGGTCATGGGCCAGCCCAATTTCGGCCGCTCGCGCGA	76	Q
923	AlaGlyAlaArgProAlaArgProGluProAspHisLeuValProArgProAlaAla	905	문 .
767	9 GCTGGAGGAAACCTTCCGCATCGG	729	γQ
904	::::::	885	퉣
728	3 CCACATGCGCGACGAAGGCGAGCACATCGT	693	Ŋ.
884	7 HlsLysSer	877	밁
592	3 CACCGAAGAGATCATCGAGGTGTGCCGGCCGCCTGAGCGCGCATGGCCGCATCTACGCCAC	633	ρ
876	0 lyalaalaThrProSerArgTrpArgProMetProAlaProLysalaala-	860	8
632	73 GGCCAGCGGCCATCGGCATTTCGACCGGCGCCTTCTACCCGCCCG	57	Qy
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SULT 6 -09-252-991A-26129 Sequence 26129, Appl1 Sequence 26129, Appl1 GENERAL INFORMATION: APPLICANT: Marc J. TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: 107 CURRENT APPLICATION CURRENT FILING DATE: PRIOR APPLICATION NUI PRIOR TILING DATE: PRIOR APPLICATION NUI PRIOR FILING DATE: PRIOR FILING DATE: PRIOR FILING DATE: NUMBER OF SEQ ID NOS SEQ ID NO 26129	CIGGG	GAAGI	igcego	lnAr	CGCCACCTTCGAA LeuArgL CAACGGCGCGCC- 	GlyLeuGlyA GlyLeuGlyA GlyLeuGlyA GlyCeuGlyA	GTGGGGCACCT
2-991A-26129 2-991A-26129, Application, INFORMATION: ANT: MATC J. Ruben OF INVENTION: ARROLO OF INVENTION: ARROLO OF INVENTION: ARROLO OF INVENTION: ARROLO OF INVENTION NUMBER: TAPPLICATION NUMBER: TILING DATE: 1998-APPLICATION NUMBER: FILING DATE: 1998-APPLICATION NUMBER: FILING DATE: 1998-FILING D	GCCAGA yProAl	AGTGATGGG	GTGC	JASnP JASnP	CTTCGAA LeuArgL CGCGCC- 	yAspAspI yAspAspI yAspAspI yAspAspI ccccrrc	CCTTC ::: avalt G yAlac
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plication US/09252991A N: N: NUCLEIC ACID ANI AMINO ACID N: AERUGINOSA FOR DIAGNOSTICS 1 107196.136 CON NUMBER: US/09/252,991A TE: 1999-02-18 INUMBER: US 60/074,788 : 1998-02-18 : 1998-07-27 NOS: 33142	CIYATGPTOALBATGATGPTOALBGLYALBATGHISATGVBLALBGLUPTO CGAGCTGGGCCAGATCGCCCCTGAGCTACGAGAAGCT 1757 GlyPTOALBATGPTOGLYATGThrAlB 1396	CAAGGAAGTGATGGGGGGGGGGCGTGCGGGGCGAAGGGCCGGAA	CGGGGCGGCGTGCCGCCCCT	CACCGGCCAGCATGCCGGCCGGCTGCTCGCACGCACGCCGCCTG	GCCCACCTTCGAACACCCTACCGAGCGCGCGCGCCGC	GlyLeuGlyAspAspLeuArgProArgArgArgGlnGluArgGlyArgProAlaGlyGly	GTGGGGCACCTTCCCGGGGGGGCTGGGGGCACTATGCGCG
INO A NOSTI	Hisa GCT 1	GCGCA	CCCAACCCTGGACGCAAACCGCTACAT rgThrArgProGlyArgHisGlnProGlu ACGGCCCACCCGATATCGTGG ::: 	GCCGC JProp WATCC	gProA	gGlnG gGCA- ::: aserH TGTTC	uPro/
	1757 1396	AAGGC	ACCCT	GTGCT roAsp GGCGT rgAsn	CGG laArg	luarg	AspleuArgAspAlaAspG CCTGTTCCCGCTGGAGAC-
E)	AlaG1	CCGGA ProG1 CTCGA	CCTGGACGCAAA ProGlyArgHis ACCCGATATCGT :::	CGCAC	-CGGCATCCATTCCGTGTACGT ATGMETPTOATGATGVATBPTO -GGTCTGGCAAGAGCAGGCGTT ::: OALAVAIAIAATGPTOVAILeu	GGCC1	uArgA rcccg
THERAPEUTIC	uPro-	A	CAAAC GH1SC TCGT SArg?	GCACO nH1so	CCATTO	rgPro	spala Spala CTGGA
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549	euArgThrSerArgAlaLysAlaLeuProArgArgArgAlaAlaValProHisGlySer	53	p	
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	::: ::: laGlnArgProAlaAlaGlyAlaAspAlaHisLeuAspGlyLeuArgLeuArgPro	393	ДD	
N	GCATCCGCGCCTGTGGGGCACCTTCCCGCGGGTGCTGGGGCACTATGC	1146	ρ	
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1145	GATCGGCTCCGACGCCTGCCGCA	1122	ρ	
372	ArgArgProValProArgLeuArgArgGlyArgHisArgProGlyIleAla	356	뭥	
1121	CTACTTCATGATGGACGAACCCGACGTGCAGCGCATCCTGGCGTTCGGCCCGACCAT	1065	Qy	
355	GlyThrAlaArgProValProProAlaArgH18AlaAlaAlaAlaGlyArgThrSer	337	뫄	
1064	GGCCGAGCGCGAAATCCAAGTACGACGTGGTGCCCGAGCTGCAGCCGGCCG	1005	Qy	
336	AlaAlaThrValAlaAlaGlyProAlaArgGlnArgHisArgArgProAlaArgLeuVal	317	фd	
1004	-GCGCGACCTGGATGAAGTCGC	957	Qy	
316	ArgGlnArgAlaAlaAlaLeuProAr	297	d	
956	CTCCACCATGCTCAAGCAGGACCGCGTGCTGCTGGCCGGACGCACCATCATCA	900	Qy	
296		277	qi	
899	GCTGGACGCGTATCCCTACGTG	873	Оy	
276	GIYGIYAFGCY8FFOAFGFFOCYSAFGALaLeuProGluProGlyGlnProGlyArgGly	707	7	

QY 330 CAGCCTGGCGCCGCTGGCGCAACCCGCCCCCCCCCCTGGACCTGCT 380	Qy 288CTCGCAGGGCGTCACCACGGTGGTCACGGGCAATTGCGGCAT 329	Oy 285 GAT 287 Db 193 GlnArgGlyAlaValProProArgGlyAspGlyThrValAspArgLeuProArgPro 212	Qy 225 CATGGACTCGCACGACGACGACGACGACTACCTGCTGAGGCGTCGCGACATGACGCCCAA 284	Qy 171 CGCCGCGCGCACACCCCGGGTCGACGTGTCGGGCCTGGTGGTCGCGCCCGGCTT 224	Qy 111 GCGGCGCGGCGACCTGGGCGTGCGCGGCGACCGCATCGGCCATCGGCGATCTGTCGGA 170	Qy 66 GCTGCTCGCGGGCGCACCCTCATCGACGGCAGCAACACACCCCGGG 110 :::	Qy 6 CCACTTGATCGCGGAAGGAGAGATTTCCATGTCCCAATCCCAATCCCAGCCCTTCGACCT 65 :::	16 Gaps: Gap	.milarity: 433.00 .milarity: 34.29% .Similarity: 29.18% h.	991A-19446 Scores: 3 888-16 Tooth		PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SET IN 60: 32107-27	AEKUGINUSA FOR DIAGNOSTICS AND THERAPEUTICS 1196.136 NUMBER: US/09/252,991A 1999-02-18 NUMBER: ES (2014 700	L INFORMATION: CANT: Marc J. Rubenfield et al. OF INFENTION: NUCLEIC ACID AND AMINO ACID SEQ		1740 CCT	1722 CGAGCTGGGCCAGATCGC	Qy 1671 GCAAGACCTGTCGCAGGCCAGGCGCATCGGGGTCTCGACCCTGTCCAAGGC 1721
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1080 CGAACCCGACGTGCAGCGCATCCTGGCGTTCGGCCCGACCATGATCGGCTCCGACGGCCT 1139	1029CGACGTGGTGCCCGAGCTGCAGCCGGCGGCGCCATCTACTTCATGATGGA 1079	978 GAGCGGGCGGACCTGGATGAAGTCGCGGCCGACGCGGCAAATCCAAGTA 1028	918 519	858 499	. 798 479	780 459		7 678 CGGCATCTACGCCACCCACATGCGCGACGAAGGCGAGCACATCGTGGCCGCGCTGGAGGA 737 :::	402		621 362		ω un	y 543GCCATGCGGGACCTGGCCGATGGAAGCCATGGCCAGCGG	y 486 GCTGCGCGCGGCGGTCATGCCGGACTTGCAGGGGCGCGCGC	y 429 CGCGTTGCGGGCCACGCCGGCGGCGTCAACGCCGCCTGTATGGTGGGCCATTCAAC 485 :::	253	233

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US-09-252-991A-30843, Application US/09252991A; Sequence 30843, Application US/09252991A; GENERAL INFORMATION: Rubenfield et al. APPLICANT: MAIC J. Rubenfield et al.; TITLE OF INVENTION: NUCLEIC ACID AND AN TITLE OF INVENTION: AERUGINOSA FOR DIAC
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             CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788
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                                                                      MAIC J. Rubenfield et al. MAINO ACID SEQUENCES RELATING AVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING AVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS ENCE: 107196.136
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US-09-252-991A-30843
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PRIOR APPLICATION NUMBER: US:
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30843
LENGTH: 663
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                                                                                                             CysSerProValAlaThrAlaProThrAlaThrCysSerProProSerAlaArgSerAla
                                                                                                                                                                                                                     TGGCCAGCGGCGCATTCGGACCGGCGCCTTCTACC-----CGCCCGCCGCCC 625
                                                                                                                                                                                                                                                                                                                                      SerAlaTrpTrpTrpLeu------AlaProAlaArgCysCysTrpProAlaProPro
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                                     TrpLysProCysAlaCysAlaLysAlaValGlySerAlaArgSerProAlaAsnAlaTrp
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	, 542	24 oAlaHisArgProSerAlaSerAlaThrGlyTrpProGlyProAlaLeuAlaCy	Db 5:
	r _. 1353	94 C	Qy 12
	524	04 yArgArgThrProAlaAlaArgArgArgSerAla	Db . 50
	1293	8	ОУ 126
	504	84 gAlaArgThrGlyIleArgArgThrAlaAlaAlaAlaCysTyrProProAlaProGl	Db 48
	1267	59TGACCGCCG	Qу 125
	. 484	64 yAlaGlyProAlaSerThrGlyArgSerArgArgArgTrpAlaAlaAlaProAlaArgAr	Db. 40
	1258	5GGGCCTGTTCCCGCTGGAG	Qу 121
	1 464	444 eAlaGlySerAlaProGlySerGlyThrAlaProArgCysHisProValArgLysAspGl	Db 4
	1214		Qy 1172
•	444	425 aAlaAspHisProAlaAlaTrpValSerAlaAlaArgArgThrSerSerAlaProIl	Db 43
•	1171		Oy 1112
	425	405 gAlaThrProAlaSerAspAlaArgArgAspSerAlaSerArgGlyArgProAlaThrAl	Db 40
	1111	GCGCCATCTACTTCATGATGGACGAACCCGACGTGCAGC	Оу 1058
	405	386 uArgArgArgValArgArgSerAlaArgArgAlaTrpArgProTrpProAlaGlyAr	Db 38
	1057	.013 GCGGCAAATCCAAGTACGACGTGGTGCCCGAGCTGCA	Оу 101
	386	371 GlyGlyTyrAlaAlaAlaProArg-AsnSerCysSerAlaGlyArgLe	Db 37
	1012	TGA	Qy 95
	370	53 ProAlaGlyProArgProSerCysThrAlaValAlaAlaTrpAlaProAlaArg	Db 35
	952	905 CCATGCTCAAGCAGGACCGCGTGCTGCTGGCCGGACGCACCATCATCA	0у 90
	352	6 ProTrpSerAlaVa	Db 33
	904	0	Ωу. 86
	335		Db 31
	859	148 CCGCCATGGCGC	Ωу 84
	315	97SerAlaThrArgLeuAlaAlaCysGlyHisAspGlyAspAlaGlyArgAlaSerGln	рь 29
	847	• ດ	Оу 80
	296	91 AlaMetProProSerThr	Db 29
	808	49 TCGGCCGCGAGCTGGACGTGCCGGTGGTGATCTCGCACCACAAGGTCATGGGCCAGCCCA	0у 74
	290		Db 271
	748	92 CCCACATGCGCGACGAAGGCGAGCACATCGTGGCCGCGCGCTGGAGGAAACCTTCCGCA	Оу 69
	270		25
-	691		Qу 65
	250	${f 31}$ Pro ${f Ala}$ AlaSer ${f Ala}$ TrpCysProThrCysAsnSerAla ${f Arg}$ ProSerAlaIle ${f Ala}$ Ser	Db 231

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CGACAACTACCTGCTCAG ::: ArgArgArgProAlaGlnPr	garge	yGlnA: GCGAT	CCCAGO		Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB:	1528 GCGTGCCGCCCCCCAACCCTGGACGCAAA :: :: :: :: :: :: :: :: :: :: :: ::	roArgA ACGCAC
TACCTO	lnPro/ TTCATO	 CTGTC	CCCTT(alaspo	נ (758		CCCCTCCCAACC : CGGCCCC	laPro GGCCG
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FroAl	GINAL GCACA	Alapr CGCCG	GCTGC	9-252	9 0	CTGGAV OALAA CCCGAV	gArgP
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CGACAACTACCTGCTCAGGCGTCGCGACATGACGCCCAAGATCTCGCAGGGCGT :::	GlnArgArgGlnProArgArgGlnAlaGlyGlnProGlyAlaAlaGlyAspHisArg CGCGCCCGGCTTCATCGACTCGCACACCCCACGA		CGATTCCCAGCCCTTCGACCTGCTGCTGCTGCGGGGGGGG	(1-1758) x US-09-252-991A-21920	Length: Matches: Conservative: Mismatches: Indels: Gaps:	CCGCT GGGCL GGGCL CCAGC GCAAC hrTh CCAGC L rgArc yla gNOSC GNOSC 91A 8	aArgProArgAlaProArgArgArgProGlyArgSerProAlaThrAlaProAlaAlaPh CTCGCACGCACGCCCCTGAGCCCGGCGCCCAGCCCTTACAATCCGGCGTGAACGGGGCG :::
GACGCC AspLeu	rogly	 rgArg GTCGA	CGGCACCCT	(1-822)	tive:	ACATGE ALGTRE LAGGAAG LAGGAAG LAGCTGT ACCTGT CG1yAla LICG 17 LICG 17 JSET 65 ACID S RICGS AN	ProAla
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Qy 816 CCGCTCGCGCGAGAC		21 POSPONON HEREOCONNECC	9
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Оу 774		12.87% Indels:	B 5
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Oy 717 CATCGTGGCCGCGC		1.19e*15 Length:	Sc
Db 336		Alignment Scores:	Al
QY 657 CCGGCCGCTGAGCGC		; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-27980	SD ,
Db 320 ArgIleProProArc		; LENGTH: 1002 ; TYPE: PRT	·· ··
QY 606 CTTCTACCCGCCGG		; NUMBER OF SEQ ID NOS: 33142 ; SEQ ID NO 27980	
Db 303 GlyArgGlyThrAre		; PRIOR APPLICATION NUMBER: US 60/094,190 ; PRIOR FILING DATE: 1998-07-27	
Qy 558 GGCCGAGGAAGCCA		; PRIOR APPLICATION NUMBER: US 60/074,788 ; PRIOR FILING DATE: 1998-02-18	
Db 283 GlyArgArgGlySe		CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18	·· ··
Оу 513		STICS AND THERAPEUTICS	
Db 263 ProTrpProLeuPro	PSEUDOMONAS	; APPLICANT: Marc J: Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO P	
Qy 512		N: 12	٠. ٠.
Db 243 AlaGlyGlyGluIl		RESULT 11 US-09-252-991A-27980	US RI
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Qy 453		Db 636 ArgTyrProHisArgArgIle	ΩŁ
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ATCGAGGTGTG 656	06 CT	0у 6
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rceaccecec 605	58 GGCCGAGGAAGCCATGGCCAG	Qy 5
 lyHisGlyArg 302		
ATGCGGGACCT 557	513GCAGCGCGCGCCCCCACCGACGAAATCGCGGCC	Qy 5
roProProGlu 282	263 ProTrpProLeuProValProGlnArgThrArgLeuPheAspProAlaP	DB 2
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US-09-252-991A-25557
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TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS.

CURRENT REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
ENGIN: 11149

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APPLICANT: Marc J.
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TYPE: PRT
                                                                                     152 ArgAlaHisArgGlnProSerAlaProValValArgArgProAlaAlaAlaGlyValAsp 171
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                                                                                                                                    CGCGGAAGGAGATTTCCATGTCCCA----ATCCGATTCCCAGCCCTTCGACCTGCTGCT
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                                                                              ValProGlyH1sArgArgAlaArgArgGluArgLeuGlnLeuArgArgGlnGlyCysArg
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| GlyHisAlaGlyGluArgArgAlaGlyGlyAlaLeu----ArgGluHisArgLeu 390
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RESULT 13 US-09-252-991A-29274 Sequence 29274, Application US/09252991A Sequence 29274, Application US/09252991A GENERAL INFORMATION: MICLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 INVABER OF SEQ ID NOS: 33142 SEQ ID NO 29274 Alignment Scores: Pred. NO.: 1.4e-15 Length: 801 Fred. NO.: 1.4e-15 Matches: 222	QY 1431 AGAGCAGGCGTTCACCGGCCAGGCCAGGCCGCGCGCGCCGACGGCCGCCGGACGCCCGAGGC 1490 Db 585	Qy 1107 GTTCGGCCCGACCATGATCGGCTCCGACCGACCGCACCGCACCGCATCCGCG 116 11 11 11 11 11 11
	Db 188 GlyArgArgLeuProGlyValleuArgArgArgLeuGlnProAspProArgArg 206 Qy 249 CAACTACCTGCTCAGGCGTCGGAACATGACGCCAAGATCTCGCAGGGCGTCACCACGGT 308	Percent Similarity: 35.15% Conservative: 29 Best Local Similarity: 31.09% Mismatches: 253 Ouery Match: 12.82% Indels: 210 DB: 10-009-782-1 (1-1758) x US-09-252-991A-29274 (1-801) Oy 15 CGCGGAAGGAGATTTCCATGTCCAATCCGATTCCCAGGCCTTCGACCTGCTGCTCGC 74

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1623 GATGGGCGCGCGCCTGCGCGCGAGCGCAAGGCCCCGGAAAATGACCCTGCAAGACCTGTC 1682
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                                                                                                 ValGlnAlaGlyTyrHisProProAspProGlyAspArgArgGlnArgAspLeuArgArg
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SEQ ID NO 26099
LENGTH: 863
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOM:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
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                                     ArgThrArgLeuLeuGlyAlaAlaProProFroGluGlyHisArgGlySerSerLeuPro
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SULT 15 -09-252-991 Sequence 16 GENERAL INFE APPLICANT: TITLE OF II TITLE OF II FILE REFERI CURRENT APPLI PRIOR APPLI PRIOR APPLI PRIOR FILLI PRIOR F	1704 794		755	1608		722	1509	1449 704	684	664 1389	1359	644	1344	1284 628	608	1251	1212	568	1185	548
RESULT 15 US-09-252-991A-16789 Sequence 16789, Application US/09252991A GENERAL INFORMATION: ITILE OF INVENTION: NUCLEIC ACID AND AMINO ITILE OF INVENTION: NUCLEIC ACID AND AMINO COURSENT APPLICATION NUMBER: US/09/252,991A CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-07-27 NUMBER, OF SEQ ID NOS: 33142 SEQ ID NO 16789 LENGTH: 774 TYPE: PRI ORGANISM: Pseudomonas aeruginosa	CTCGACCCTGTCCAAGGCCGAGCTGGGCCAGATCGCCC	GACCCTGCAAGACCTGTCGCAGG 	ProG	: Description		Thrargargalaarg	ATCCGGCGTGAACGGGGGGGGGGGGGGGGGCGCGCCCCCCCC	CCAGCATGCCGGCCTGCTCGCACGCACGCCCTGAGCCCGGCGCGCGC		H18H18ArgArgGlnProArgH18ArgProGlyAspSerProAlaArgArgAlaArgTrp CGGCATCCATTCGTGTACGTCAACGGCGCGCGCTTTGCCAACACACAC	CACCTIC	ProGlnArgGlnArgGlnGluAsnGlyAspAlaHisValThrAlaArgGlnAs	GGTGGCCGATACCGCyou you you want you set to Alac		SerArgArgi	чтиетурго:	CCTGGGCCTGTTCCCGCTGGAGACGCCGGTATGGAAGAT	 		ThrGlyArgGlyHisProArgArgArgGlnArgProGlyArgArgGlnPheArgHisAla
789 IAPPLICATION TON: TON: TON: TON: NUCLE: TION: AERUG: 107196.136: 107196.136: 107196.139- CON NUMBER: TON NUMBER: TON NUMBER: TON NUMBER: 1998-02 ID NOS: 3314	TCCAAGGCC	lyAlaGlyL	rgGlyGlyG	-CGTGGGCAAGGGAAGTGATGGGGGGGGGGGGGGGGGGGAAGGGCGGGAAAAT	rgArgThrL	laArg	AACGGGGCG	egcccccan	lyAspArgo	rgGlnProp	-CACCTTCGAACACCC	 	ACCGC	CAGCTGCAC	GlyPr	Inralaala	TTCCCGCTC	AspGlyArgi		GlyH1sPro
cation US/09252991A Rubenfield et al. NUCLEIC ACID AND AMINO ACID AERUGINOSA FOR DIAGNOSTICS / 196.136 199-02-18 1999-02-18 MBER: US 60/074,788 M1998-07-18 M1998-07-27 1998-07-27 1998-07-27 1998-07-27 1998-07-27	GAGCTGGGC 	GACCTGCAAGACCTGTCGCAGGCCAGCGGCATCGCGGT 	luAlaGlyA	ATGGGCGCG	euArgArgA		GCGTGCCGC	CTCGCACGC	lyGluGlu	rgHisargi GTCAACGG		luAsnGly	Set of Aut A	GCCGGGTA	ProArgPro	зтуктасту	GAGACGGC	ArgHisArg		ArgArgArg
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SEQ SEQ	CC 1741	GTCGCAGGC	LeuArgPro	CGCCGAGC	-CAATACGGCCCACCGATAT ::: gArgAlaGlyGlnGlnArgArg	 -ArgAlaGlyArgGlyGlyHis	AACCCTGG/	CTGAGCCC	CreeCAAe ::: AlaSerGl	SerProAl		ValThrAl	PIOALa	CCTGGTGG	TrpArgAl	1AspGlyTh	GAT	161yArgAr	-GCGGGTGCTGGGGCACTATGCGCGCGA	oGlyArgAr
SEQUENCES RELAT		CCAGCGGCATCGCGGT roAlaGlnGluArgG) AspValPr	CAAGGCCC	CACCCGATA GlnArgA	lyArgGlyG	ACGCAAAC	GCGCCAGO	AGCAGGCG 	aArgArgA	TACCGAGCGCGCCGC	aArgGlnA		TGTTCGAC	eccectic aglyAlag	rProAlaG		gGlyArgT	GGCACTAT	gGlnPheA
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US-09-252-991A-16789

Ş 밁 Š 밁 S 밁 문 US-10-009-782-1 (1-1758) x US-09-252-991A-16789 (1-774) Query Match: Percent Similarity: Best Local Similarity: Pred. No.: Alignment Scores: 307 287 AlaAspProArgGlyH18ArgLeuGlnAlaH18ArgGlnAlaAlaArgGlyH18H18Arg 306 645 CATCGAGGTGTGCCGGCCGCTGAGCGCGCATGGCGGCATCTACGC--------273 HisargGly-------GlySerArgHisAlaArgProAlaGlyIleAsp 286 253 HisargieuProHisHisHisAspGlnArgProArgArgAlaArgLeuGlyArgArgArg 272 603 CGCCTTCTACCC-------GCCGCCGCCGCCGCCGCCACCAAGAGAGAT 644 233 HisGlyLeuAspGlnGlyArgGlyTrpGlnAspLeuArgLeuProArgHisProGlyArg 213 GlnArgGlyThrAlaGlyHisArgHisLeuProProGlyGlnProGlyValProGlyPro 501 CATGCCGGACTTGCAGCGCGCCGCCAC---CGACGAGGAAATCGCGGCCATGCGGGACCT 557 194 AlaGlnArgArgThrLeuArgLeuProAlaLeuGlyPro---GluArgLeuArgGlnLeu 212 444 GCCGGCGGCCGTCAACGCCGCCTGTATGGT----GGGCCATTCAACGCTGCGCGCCGCGGT 500 174 AspGlyArgGlnValArgGlnArgIleGlyLeuArgThrGluArgArgAspArgAspAla 193 399 157 339 142 279 GCCCAAGATCTCGCAGGGCGTCACCACGGTGGTCACGGGCAATTGCGGCATCAGCCTGGC. 338 219 CGGCTTCATCGACTCGCACACCCACGACGACAACTACCTGCTCAGGCGTCGCGACATGAC 278 112 AlaGinGlyAlaProPheArgProArgAspProValProProGlyAlaSerProAspAla 131 183 -----CACCCGGGTCGACGTGTCGGGCCTGGTGGTCGC-----GCC 218 123 CCTGGGCGTGCGCGACCGCATCGCCGCCATCGGCGATCTGTCGGACGCCGCCGCGCA 182 92 ProAlaLeuGlyGlyArgGlnHisArgHisArgArgArgProGlnGlyProArgArgLeu 111 18 GGAAGGAGATTTCCATGTCCCAATCCGATTCCCAGCCCTTCGACCTGCTGCTCGCGGG 72 ProAspProGlyArgSerArgGinAlaAlaAspValAlaGluGlyProAlaGlyLysPro 91 58 GlyArgGlnAsp-------LeuProLeuLeuGlnProProGlySerArg 71 H1sArgProGlyAlaAspArgH1sAlaAspAlaAlaGlnGluGlyArgGlyGlyGluIle 326 CATCGGCCGCGAGCTGGACGT------CCGTTTCGAGCGCTTCGCCGACTACCTGGA------CGCGTTGCGGGCCCAC 443 -----AlaGluAspGinProAlaValAlaGlyGlyPro---GlyH1sArgProLeuGly 173 GCCGCTGGGCGCACGCCAACCCGCCCGCCCCCTGGACCTGCTGGACGAAGGCGGCTCTTA 398 4.81e-15 413.50 33.08% 28.70% 12.53% Length:
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-TRANS-human40.cd1 -LIST-45 -DCCALIGN-200 -THR_SCORE-pct -THL_MAX-100
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ALIGNMENTS

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6.66e-07 310.00	PRT SM: Pseudomonas aeruginosa 719-277	FAST ID NOS: 437 FASTSEQ for Windows Version 277 558	FLICATION NUMBER: US 09/199,637 LING DATE: 1998-11-25 PLICATION NUMBER: US 60/066,517 LING DATE: 1997-11-25	ERENCE: 00786/361003 APPLICATION NUMBER: US/09/975,719 FILING DATE: 2001-10-10	: Ausubel, Frederick M. : Rahme, Laurence G. : Rahme, Laurence G. : ROTHERLENCE ASSOCIATED NUCLEIC TIVENTION: VIRGLENCE ASSOCIATED NUCLEIC	19-277 277, Application US/09975719 on No. US20030022349A1	CGCACG 1479 ::: ArgSer 548	GCGCGCCGGTCTGGCAL yGlnIleAlaValAsp	CCGCCACCTTCGAACAC ::: ::: etSerThrTyrGluGlu	AGCTGCAGGCCGGGTA::: ::: sulleAlaGluGlySes	CGGTATGGAAGATGAC ::: :: :: etIleAlaHisLeuTh	CCTTCCCGCGGTGCT rPheThrArgTyrLe	CCATGATCGGCTCCGA sMetAlaGlySerAs	GCGCCATCTACTTCAT ; ; erCysIleMetHisVa	GGCCGAGCGCGAATCCAAGTACGACGTGGTGCCCGAGCTG 3.1	hrAsnGluProSerIL	ysGlyCysAspGlyG1	hrLeuLysArgLeuGl
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ω o ₀	pplication US/09 US20030022349A1 TION: ubel, Frederick hme, Laurence G. TION: VIRULENCE- TION: SEQUENCES: 000786/361003 ATION NUMBER: US 0 DATE: 2001-10: ION NUMBER: US 0 ATE: 1998-11-25 ATE: 1997-11-25 ID NOS: 437 ID NOS: 437 ID NOS: 437 SEQ for Windows SEQ for Windows	GCAC ::	gcec - ye1	etse	AGCT :: euIl	CGGT etI1	hr Pl	1sMe	ercy	1909 1919	hrA
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CURRENT APPLICATION NUMBER: US/09/801,368

CURRENT FILING DATE: 2001-03-07

PRIOR APPLICATION NUMBER: US 09/487,558

PRIOR FILING DATE: 2000-01-19

PRIOR APPLICATION NUMBER: US 60/160,587

PRIOR FILING DATE: 1999-10-20

NUMBER OF SEQ ID NOS: 440
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SEQ ID NO 108
LENGTH: 1367
TYPE: PRT
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                        AGATCATCGAGGTGTGCCGGCCGCTGAGCGCGCATGGCGGCATCTACGCCACACATGC
                                                    ---ProSerSerSerThrThrGluSerSerSerAlaProAlaProThrProSerSerSer
                                                                              GCGCCATCGGCATTTCGACCGGCGCCTTCTACCCGCCGCCGCCGCCGCCCACCACCGAAG
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RESULT 4
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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michae

APPLICANT:

Lodes, Michael J Secrist, Heather

Darin R

QY 542 CGCCATCCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCCATCGGCAT	Qy 482 CAACGCTGCGCGCGGGTCATGCCGGACTTGCAGCGCGCCGCCGCCACCGACGAGGAAAT Db 1490ThThThrThrPhrProProProThThrThrThrPhrProProProThThrThrThrPhrProProProThThrThrThrPhrProProProThThrThrThrPhrProProProThThrThrThrPhrProProProThThrThrThrPhrProProProThThrThrThrPhrProProProThThrThrThrPhrPhrProProProThThrThrThrPhrProProProThThrThrThrPhrPhrProProProThThrThrThrPhrPhrProProProThThrThrThrPhrPhrProProProThThrThrThrThrThrThrThrThrThrThrThrThrTh	Qy 422 ACCTGGACGCGTTGCGGGCCACGCCGGCCGGCCGTCTATGG	2 CCCCCCCCTGGACCTGCACGAAGGCGGCTCTTACCGTTTCGAGCGCT	302 CCACGGTGGTCACGGGCAATTGCGGCATCAGCCTGGCGCGCTGGCGC	Db 1449 LeuProThrThrThr	1435	122 ACCTGGGCGTGCGC	62 ACCTGCTGCTGCGGGGGGGCACCCTCATCGACGGCAGCAGCACACCCCGGGG	1383	US-10-009-782-1 (1-1758) x US-10-025-380-1068 (1-5179)	Alignment Scores: 4.4e-06 Length: 5179 Score: 289.50 Matches: 146 Percent Similarity: 32.92% Conservative: 41 Best Local Similarity: 25.70% Mismatches: 164 Query Match: 8.78% Indels: 217 DB: Gaps: 29	Thomas S. Darrick COMPOUNDS FOR IMMUNOTHERAPY AND OF COLON CANCER AND METHODS FOI 121.471C14 NUMBER: US/10/025,380 : 2001-12-19 S: 1129 or Windows Version 4.0	APPLICANT: Stolk, John A. APPLICANT: Wang, Tongtong APPLICANT: Jing, Yuqiu APPLICANT: Smith, Carole L. APPLICANT: King, Gordon E. APPLICANT: Wang, Aijun APPLICANT: Wang, Aijun APPLICANT: Skeiky, Yasir A. W. APPLICANT: Fanger, Gary R.
CGCCATCGGCATTTCGACCG 601	GGCCACCGACGAGGAAATCG 541 coProProThrThrThrPro 1500	CGCCTGTATGGTGGGCCATT 481 roThrThr	TTTCGAGCGCTTCGCCGACT 421 ::: ThrProSerProPro 1473	GCTGGCGCACGCCAACCCGC 361 ThrThrThrThr 1463	CAAGATCTCGCAGGGCGTCA 301	CTTCATCGACTCGCACACCC 241 :::::: leThrThrThrThrPro 1448	TCTGTCGGACGCCGCCGCC 181 hrThrThrProProPro 1434	CACCCCGGGGGGGGGGGGCG 121		179	517 146 e: 41 164 217	ν ₃ 29	

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	ProThrThrMetThrTroSerProThrThrThrProSerSerProIle	roSer				ThrLeuproproThrThrThr				roThrThrThrThrThrProProProThrThrThrProSerProProThrThrThr	CTACTTCATGATGGACGAACCCGACGTGCAGCGCATCCTGGCGTTCGGCCCGA		ATCCAAGTACGACGTGGTGCCCGAGCTGCAGCCGGCCGGCCGCCCA	hrThrProSerPro	CAAGCCCTTCCCCGAACTGAGCGGGGCGCGACCTGGATGAAGTCGCGGCCGAGCGCGCG	erProProProThrThrThrThrProProProThr	CTCCACCATGCTCAAGCAGGACCGCGTGCTGCTGGCCGGACGCACCATCATCACCTGGT		CGAGGCCGCCATGGCGCGCGAGGACGTCTCGCTGGACGCGTATCCCTACGTGGCCC	:: :::	GCACCACAAGGTCATGGGCCAGCCCAATTTCGGCCGCGCGCG	roproproThrThrProSerproProThr	rggccgcgctggaggaaacctttccgcatcggccgcgagctggacgtgccggtggtgatcat	SerProProThrThrThrThrThrThrThrThrThrThrThrThrThrT) GCTGAGCGCGCATGGCGGCATCTACGCCACCACATGCGCGACGACGACGAGCGACCGAC	AlaSerThrThrLeuProProThrThrThrPro	3CGCCTTCTACCCGCCCGCCGCCCGCGCCACCAAGAGATCATCGAGGTGTGCCGGC		TATAL THE THE TATAL TO THE TATAL TO THE TATAL TO THE TATAL THE TAT		CAACGCTGCGCGCCGCCGCTCATCCCGGACTTTCCACCCCCCCC		ACCTGGACGTTGCGACGTGACGCACACGCACACGACACACAC	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

	Score: 7.81e-06 Length: 941 Score: 285.50 Matches: 137	US-10-124-557-14 DESCRIPTION: SEQ ID NO: 14:		TYPE: amino acid	SEQUENCE CHARACTERISTICS:	INFORMATION FOR SEO ID NO: 14.		REGISTRATION NUMBER: 31,822	ATTORNEY/AGENT INFORMATION: NAME: Cserr, Luann	FILING DATE: 08-AUG-1989	1	FILING DATE: 29-JUN-1990	FILING DATE: 18-JAN-1991	PRIOR APPELICATION CONKNOWN>	FILICATION NUMBER: US/10/124,557 FILICATION NUMBER: US/10/124,557	CURRENT APPLICATION DATA:	SYSTEM: F	COMPTIED TOWN:	COMPUTER READABLE PODM.	STATE: Washinger Commert F C	STREET: 87 CambridgePark Drive CITY: CambridgePark Drive	ONDENCE ADDRESS:	: Megaka		S		<pre>; Sequence 14, Application US/10124557 ; Patent No. US20020137894A1</pre>	55	Db 1764 SerIleThrProProThrPheSer 1771	1586	1745 ThrThrLeuProProThrThrThrSerSerProLeuThrThrThrProLeuProPro	1526 CGGCGTGCCGCCCCCAACCCTGGACGCAAACCGCTACATGGCCCCCCCC		UY 1406 ACCTCAACGGCGCCGGCTCGGCAAGAGCAGGCGTTCACCGGCCAGCATGCCGGCCG	
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		Ov 911 TOBACCACCACCACCACCACACACACACACACACACACACA	375 L	QY 851 CCATGGCGCGACGACGTCTTCGTTCGTTCGTTCGTTCGTT		ATTTCGGCCGCTCGCGCGAGACGCTGCCGCTGATCGAGGCCG						QY 614 CGCCCGCCGCCCCCACCACCGAAGAGATCATCGAGGTGTGCCGGCCGCTGAGCG 670	Db 294 ThrThrProLysGluProAlaProThrThrProLysGluProAlaProThrThr 311	554	281	QY 494 CCGCGGTCATGCCGGACTTGCAGCGGCGCCCGCCGACGAAGGAAATCGCGGGCCATGCGGG 553	271	443	251		239	323		229 Alabromhumhu	263	217	203	202	٦ د ۸	_	92	167	12 Gaps:	Percent Similarity: 33.50% Conservative: 60 Best Local Similarity: 23.30% Mismatches: 240 Query Match: 8.65% Indels: 151	

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LysGluThrAlaProThrThrProLysLysLeuThrProThrThrProGluLysLeuAla

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1505 TACAATCCGGCGTGAACGGGGGGGGGGGGCGCCCCCCCCAACCCTGGACGCAAACCGCT
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                                                                                                                                                                               TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluProAlaProThrThrProLysLysProAlaProLysGluLeuAlaProThrThrThr 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGCCAGCG---GCATCGCGGTCTCGACCCTGTCCAAGG-----CCGAGCTGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProAla----ProLysGluLeuAlaProThrThrLysGluProThrSerThr---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LysGluProAlaProThrThrProLysGlyThrAlaPro---ThrThrLeuLys
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Best Local Similarity:
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No.
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                                                                                                                                                                                                                                           310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 ACGGCAGCA-----ACACCCCGGGGCGGCGCGCGACCTGGGCGTGCGCGGCGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 CCATGTCCCAATCCGATTCCCAGCCCTTCGACCTGCTGCTCGCGGGGGGGCACCCTCATCG
                                           GluProAlaProThrThrProLysGluProThrProThrThrProLysGluProAlaPro
                                                                                          ACGAAGGCGGCTCTTACCGTTTCGAGCGCTTCGCCGACTACCTGGACGCGTTGCGGGCCA 442
                                                                                                                                                                                                                                  AlaProThrThr-----ProLysGluProAlaPro-----
                                                                                                                                                                                                                                                                              GGCGTCGCGACATGACGCCCAAGATCTCGCAGGGCGTCACCACGGTGGTCACGGGCAATT 322
                                                                                                                                                                                                                                                                                                                                                                        GCCTGGTGGTCGCGCCCGGCTTCATCGACTCGCACACCACGACGACGACAACTACCTGCTCA 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
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FILING DATE: 18-JAW-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
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33.50%
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Matches:
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RESULT 8 US-10-124-557-84

1733 AGATCGCCCTGAGCTACGAGAAGC 1756

609 LysGlyProThrSerThrThrSer 616

1685

1625

561

ThrThrProLysGluProAlaProThrThrPro----

1565

546

1445

510

1385

1268

471

1208

Sequence 84, Application US/10124557 Patent No. US20020137894A1 GENERAL INFORMATION:

APPLICANT: Turner, Katherine Clark, Stephen C.

Jacobs, Kenneth Hewick, Rodney M. Gesner, Thomas G.

CORRESPONDENCE ADDRESS:

ADDRESSEE:

STREET: 87 CambridgePark Drive

Genetics Institute,

Inc.

COUNTRY: U.S.A. ZIP: 02140 STATE: Massachusetts CITY: Cambridge

		516 1091 534 1148 1148 550 1208		·	
Alignment Scores: 7.73e-06 Length: 1038	APPLICATION NUMBER: US 07/390,901 FILING DATE: 08-AGG-1989 NAME: CSETY INFORMATION: NAME: CSETY LUAND REGISTRATION NUMBER: 31,822 REFERENCE/DOCKET NUMBER: GI 5190 TELEPHONE: (617)876-1170 TELEPHAN: (617)876-5851 SEQUENCE CHARACTERISTICS: LENGTH: 1038 amino acids TYPE: amino acid TOPOLOGY: linear SEQUENCE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 74: US-10-124-557-74	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 APPLICATION DATA: APPLICATION UNMER: US/10/124,557 FILING DATE: 16-Apr-2002 CLASSIFICATION: <unknown> PRIOR APPLICATION NUMBER: US 07/643,502 FILING DATE: 18-JAN-1991 APPLICATION NUMBER: US 07/546,114 FILING DATE: 29-JUN-1990 APPLICATION NUMBER: US 07/457,196 FILING DATE: 29-DEC-1989</unknown>	. : !!	Db 670 GluProAlaProThrThrProLysLysProAlaProLysGluLeuAlaProThrThrThr 689 Qy 1733 AGATCGCCCTGAGCTAGGAGAC 1756 Db 690 LysGlyProThrSerThrThrSer 697 RESULT 9 US-10-124-557-74 Sequence 74, Application US/10124557 Fatent No. US20020137894A1 GENERAL INFORMATION: APPLICANT Turner, Katherine Clark Greene	Db 627ThrSerAspLysProAlaProThrThrProLysGlyThrAlaPro 641 Qy 1565 ACATGGCCCTCCCTCCGCAATACGGCCCACCCGATATCGTGGGCAAGGAAGTGA 1624

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DOBJESTITIETTY: 23.30% MISMATCHES: 24.000 Simulative: 26.000 Simulative: 26.000 Match: 12.000 Mismatches: 24.000 Mismatches:	ΔĀ	Db (νQ	B 24	, 윰	Qy	문	γQ	р .	φ	문 4	2 8	3 1	Ş	용	γ0	망	γ	₽	Qγ	Дb	Qy .	Db	νQ	뭥	₽	₽ 5	g B	, Q	ઠ	Qy	US-1	Percer Best 1 Query DB:
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rity: 23:30% Mindels: 240 1-1758) x US-10-124-557-74 (1-1038) CCAATCCCATTCCCAGCCCTTCGACCTGCTGCTGCGGGGGCACCCTCATCG CCA	GAAC	roThrī	CAAGCA	TGG Lys	roLysc	GGTCAI	luPros	GGAGGI		GCATG	hrLys			1 G		cecee	μŢ	ဂ္ဂ	luPro	ര		CGGC	laPr	GCGTC		CCIG	# \$	ThrLys	ACGGC!	ProTh	CATG	782-	milari Simil h:
33.50% CONSERVACIONES: 240 8.55% Indels: 241 24	GAGCG	hrThri	GACCO	roAlar	luPro	GGGCC	erPro	MACCE	(hrThr)	CGGCA	luPro	SKTOTAR	2	GAG		TCATGC	ດ	.G	н	ရှိ	;	AGCC	ThrThr	GCGAC	;	ដ	GluPro	SerAla	- ;	ProTh	CCCAA	1-17	y: rity
Conservative: 60 Mismatches: 240 Indels:	GCGCG	ysLys	CGTGC	GGACG	AlaPro	:8		ဂ္ဂ	LysGlu	TCTACO	SerPro	GIUPI	:: ; :: ;	AAGCC	1	CGGAC	roAl	;	Thrib	CTTAC		TGGC		GACG		20	aPr	2			වූ	8) x	12.33
nservative: 60 dels: 240 74 (1-1038) 74 (1-1038) 76 (1-1038) 77 (1-1038) CGCGGCTGCTCGCGGGGCGCGCCGCCGCGCGCGCGCGC	ACCTG	ProAla	Tecre	# . G		TIC		ດ	 ProAl	CCACC	dir.	aPr		Augurt Fr	V.1	TGCAG	aProTh	-ccerc	rProLy	CGTTTC	:	ရှိ	:	င္ပ		GGCTTC	GATC	rThri	— <u>₹</u>	Lyss	4000	-10	* O O O
nservative: 60 dels: 240 74 (1-1038) 74 (1-1038) 76 (1-1038) 77 (1-1038) CGCGGCTGCTCGCGGGGCGCGCCGCCGCGCGCGCGCGC	ATGAA	ProTh	3CCGGA	CTGGAC DLYSG1		GCCGC		CGCGAG	aProTh	CACATO	rProLy	OThri	- AGC 66	200000	46 D	cecec	:	AACGC	3 G11	ດ	Thri	GCGCA		≫	ij i	ATCG	GTCGGA	roLysG		erAlaF	GCCCTI	124-	
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	GCGG	₩ - 6	ລ	GIGGCO		CIGCC	sGluP	GTGGT	TALAP		oThrT	ດ	2			GAAAT		GGCCA	rProL	CTGGA	COALaF	20000		င်္ဂ	laproj		CACCC uPro/	hr	ดี	ysGlui	cecee		
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SULT 10 10-124-557-58 -10-124-557-58 Sequence 58, Application US/10124557 Patent No. US20020137894A1 GENERAL INFORMATION: APPLICANT: Turner, Katherine APPLICANT: Turner, Katherine Hewick, Rodney M. Gesner, Thomas G. Gesner, Thomas G. TITLE OF INVENTION: Megakaryo NUMBER OF SEQUENCES: 143 CORRESPONDENCE ADDRESSE: ADDRESSE: Genetics Inst. STREET: 87 CambridgePark CITY: Cambridge STATE: Massachusetts COUNTRY: U.S.A.	1685 AGGCCAGCGGCATCGCGGTCTCGACCCTGTCCAAGG	1565 ACATGGCCCCTCCCCTCCGCTASpLysProAlaProThrThrProLysGlyThr 1626 ThrThrProLysGluProAlaProThrThrPro- 1625 TGGGCGCGCTGCGCGCGCGAATACGGCCCACCCGATATCGTGGGCAAGG 111 112 1625 TGGGCGCGCTGCGGCGCAAGACGCCCGGAAAATGACCCTGCAAGACC 1625 TGGGCGCGCGCTGCGGCGCCGAAGGCCCGGAAAATGACCCTGCAAGACC 1637LysGluProAlaProThrThrProLysGlyThrAlaProThrThr	1385 CCGCCGGCATCCATTCCGTGTACGTCAACGGCGCGCGCCTGGCAAGAG	1208 GCGACCTGGGCCTGTTCCCGCTGGAGACGGCGGTATGGAAGATGACCGGCCTGACCG 535	1031 1031 500 1091 518 1148
	17			754 1267 1267 111 127 127 127 127 127 127 127 127 12	1a 499 CG 1090 Hr 517 CG 1147

1140 137 60 240 151

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; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: US-10-124-557-104
    Alignment Scores:
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US-10-124-557-104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 104, Application US/10124557 Patent No. US20020137894A1 GENERAL INFORMATION:
                                                                                                                                                                        TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1733 AGATCGCCCTGAGCTACGAGAAGC 1756
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                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Turner, Katherine Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluProAlaProThrThrProLysLysProAlaProLysGluLeuAlaProThrThrThr 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGCCAGCG---GCATCGCGGTCTCGACCCTGTCCAAGG------CCGAGCTGGGCC 1732
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                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                        TOPOLOGY: linea
                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                       NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                      LENGTH: 1140 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF INVENTION: Megakaryocyte Stimulating Factors R OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jacobs,
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|---ThrSerAspLysProAlaProThrThrProLysGlyThrAlaPro
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                                                                 SEQ ID NO:
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Best Local Similari
Query Match:
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594 ProThrThrLysLysProAlaProThrAlaProLysGluProAlaProThrThrPro 613
                                           911 TCAAGCAGGACCGCGTGCTGGCCGGACGCACCATCATCACCTGGTGCAAGCCCTTCC 970
                                                                                                                                 851 CCATGGCGCGCCAGGACGTCTCGCTGGACGCGTATCCCTACGTGGCCGGCTCCACCATGC 910
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                                                                                          LysLysProAlaProThrThrProLysGluProAlaProThrThrProLysGluProAla
                                                                                                                                                                                                                        AGGTCATGGGCCAGCCCAATTTCGGCCGCTCGCGCGAGACGCCTGCCGCTGATCGAGGCCG 850
                                                                                                                                                                                                                                                                                                         TGGAGGAAACCTTCCGCATCGGCCGCGAGCTGGACGTGCCGGTGGTGATCTCGCACCACA 790
                                                                                                                                                                                                                                                                                                                                                       ProThrThrTysGluProAlaProThrThrThrLysSerAlaProThrThrProLys
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Conservative:
Mismatches:
Indels:
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1685 AGGCCAGCG---GCATCGCGGTCTCGACCCTGTCCAAGG------CCGAGCTGGGCC 1732
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                                                                                                                                                                                                                                                                                                                                                                                                                               GluProAlaProThrThrProLysLysProAlaProLysGluLeuAlaProThrThrThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGCCGGCATCCATTCCGTGTACGTCAACGGCGCGCGCGGTCTGGCAAGAGCAGGCGTTCA 1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProAla----ProLysGluLeuAlaProThrThrThrLysGluProThrSerThr---. 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGGCCAGCATGCCGGCCGCGTGCTCGCACGCACGCCGCCTGAGCCCGGCGCCCAGCCCT 1504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProLysGlyThrAlaPro---ThrThrLeuLysGluProAlaProThrThrProLysLys 727
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
US-10-124-557-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
316 GluProAlaProThrThrProLysGluProThrProThrThrProLysGluProAlaPro
                                    383 ACGAAGGCGGCTCTTACCGTTTCGAGCGCTTCGCCGACTACCTGGACGCGTTGCGGGCCA 442
                                                                                           304
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FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY, AGENT INFORMATION:
                                                                                                          GGCGTCGCGACATGACGCCCAAGATCTCGCAGGGCGTCACCACGGTGGTCACGGGCAATT
                                                                                                                                                                                                                                                                                                                                                                        ThrLysSerAlaProThrThrProLysGluProAlaProThr-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1270 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2002
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                                                                                                                                                      --ProLysGluProAlaPro---
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                                                                      -ThrThrProLysLysProAlaProThrThrProLys 315
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Indels:
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Sequence 44, Application US/10124557 Patent No. US20020137894A1 GENERAL INFORMATION:

APPLICANT:

Turner, Katherine Clark, Stephen C. Jacobs, Kenneth Hewick, Rodney M. Gesner, Thomas G.

TITLE OF INVENTION: Megakaryocyte Stimulating NUMBER OF SEQUENCES: 143

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive

Inc.

STATE: Massachusetts

10-124-557-44

1733 AGATCGCCCTGAGCTACGAGAAGC 1756

808 LysGlyProThrSerThrThrSer 815

1565

745

760

ThrThrProLysGluProAlaProThrThrPro-----

771

1505

	6 1	CCGGCCAGCATGCCGGCGTGCTGGCACGCACGGCCGGCCTGAGCCCGGCGCCAGC 	1445 594
	A 1444		1385 575
)G 1384 Lr 574	TGTTCGACCCGGCCACGGTGGCCGATACCGCCACCTTCGAACACCCTACCGAGCGCG	1328 555
	3G 1327		1268 536
	2G 1267 	GUGACCTGGGCCTGTTCCCGCTGGAGACGGCGGTATGGAAGATGACCGGCCTGACCGCCG	555
	534		534
	3C 1207	ACGAGCGCCCGCATCCGCGCCTGTGGGGCACCTTCCCGGGGTGCTGGGGCACTATGCGC	1148
	CG 1147	TGCAGCGCATCCTGGCGTTCGGCCCGACCATGATCGGCTCCGACGGCCTGCCGCAThrProGluGluProThrProThrProGluGluProAlaProThrThr	518
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	CG 850	AGGTCATGGGCCAGCCCAATTTCGGCCGCTCGCGCGAGACGCTGCCGCTG	791
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		4 CGCCCGCCGCCGCCGCCACCACCGAACAACACATCATCATCATCATCATCATCATCATCATCAT	₽ .
		ACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCATCGGCAT	y 55
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		94 CCGCGGTCATGCCGGACTTGCAGCGCGCCGCCGACGACGAAATCGCGGCCATGCGGG	у 49
	3CG 493	<pre>### CGCCGGCGGCGTCAACGCCGCCTGTATGGTGGGCCATTCAACGCTGCGCG ##############################</pre>	y 443 b 336
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CORRELE REALIMENTS MEDIUM TYPE: COMPUTER: IB OPERATING SY SOFTWARE: PA FULING DATE: FILING DATE: PRIOR APPLICATION FILING DATE: APPLICATION INAME: CSerr, REGISTRATION REFERENCE/DO TELEPHONE: (61) INFORMATION FOR SEQ IB SEQUENCE CHARACTER LENGTH: 1311 INFORMATION FOR SEQ IB SEQUENCE CHARACTER TYPE: amino. a TOPOLOGY: 111 MOLECULE TYPE: pro SEQUENCE DESCRIPTI 10-124-557-42	RESULT 13 US-10-124-557-42 US-10-124-557-42 Sequence 42, Appli Patent No. US20020 GENERAL INFORMAT APPLICANT: NUMBER OF IN NUMBER OF S CORRESTED CORRESTED STREET COUNTR STREET COUNTR TILE OF IN NUMBER OF S CORRESTED COUNTR STREET COUNTR ZIP: OF SIRE	1505 TACANTCGG 611 1565 ACATGGCCCC 1565 ACATGGCCCC 1616 ThrThrProl 1625 TGGGCGCGCG 1637
COMPUTER: IDM PC COMPATIBLE FURM: COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOSTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2002 CLASSIFICATION NUMBER: US 07/643,502 FILING DATE: 18-JAN-1991 APPLICATION NUMBER: US 07/546,114 FILING DATE: 19-JUN-1990 APPLICATION NUMBER: US 07/457,196 FILING DATE: 29-JUN-1990 APPLICATION NUMBER: US 07/457,196 FILING DATE: 29-DEC-1989 APPLICATION NUMBER: US 07/457,196 FILING DATE: 08-AUG-1989 APPLICATION NUMBER: US 07/390,901 FILING DATE: 08-AUG-1989 APPLICATION NUMBER: US 07/457,196 FILING DATE: 08-AUG-199 APPLICATION NUMBER: US 07/457,196 APPLICATION	lication 20137894# ATION: Turner, Clark, Jacobs, Hewick, Gesner, Gesner, Gesner, Gesner, Gesner Gesser Gess	TACAATCCGGCGTGAACGGGGCGGCGCCCCCCCAACCCTGGACGCAAACCGCT
		CGCT 1564 aPro 625 GTGA 1624 636 636 TCGC 1684 LLys 653 uLys 653 GGCC 1732

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Best Local Similarity:
Query Match:
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FILING DATE: 18-7AN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1999
APPLICATION NUMBER: US 07/457,196
FILING DATE: 99-DEC-1999
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CSerr, Luearn
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-1170
SEQUENCE CHARACTERISTICS:
LENGTH: 1313 amino acids
263 GGCGTCGCGACATGACGCCCAAGATCTCGCAGGGCGTCACCACGGTGGTCACGGGCAATT 322
                                                                                                                                                                                                                                              203 GCCTGGTGGTCGCCCCGGCTTCATCGACTCGCACACCACGACGACAACTACCTGCTCA 262
                                                                                                                                                                                                                                                                                    310 ThrLysGluProAlaPro-----ThrThrProLysGluProAlaProThr-----
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APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION DATA:
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COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPTWARE: Patentin Release #1.0, Version #1.25
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285.50
33.50%
23.30%
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                                                        --ThrThrProLysLysProAlaProThrThrProLys 358
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Conservative:
Mismatches:
Indels:
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Db 359 GluProhlaProflurDrePoLysGluProhlaProflurProLysGluProhlaPro 378 Qy 443 GGCGGCGG	_	_	_	_			.:																														
43 CGCCGGCGG	ğ	Ωy	g	Ϋ́	B	VΩ	ď	Qγ	8	Qy	망	Qy.	당	Qy	В	δĀ	g	δÃ	D D	VΩ	용	Q.	ర్జ	Qγ	B	δÃ	DЬ	Qy	g	Qy	뭥	VΩ	망	γQ	D _D	δ	g
GluProAlaProThrThrProLysGluProThrProThyProLysGluProAlaPro CGCCGGGGGG	37	445			98	328	79	8	578	1208	577	1148	561	1091	543	1031	523	971	503	911	.483	851	7	791	0	731	440	671	420	614	402	UI	∞	494	7	443	359
		AGCATGCCGGCCGCGTGCTCGCACGCACGGCCGCCTGAGCCCCGGCGCGAGCCCT 15	Lys	TCA		_		rescossecessecaserseassecesseraerroscesacerserss 1		CGACCIGGGCCIGTICCCGCIGGAGACGGCGGTATGGAAGATGACCGGCCIGACCGCCG	LT.		hrProGluGluProThrProThrThrProGluGluProAlaProThrThr 5	GGCTCCGACGGCCTGCCGCACG	u			_	LD :		::: ThrProLysGluProAlaProThrThrProLysGluProAla	TCTCGCTGGACGCGTATCCCTACGTGGCCGGCTCCACCATGC	::: ThrThrPro	GCGCGAGACGCTGCCGCTGATCGAGGCCG	luProSerProThr	J		~	hrLysGluProSerProThrThrProLysGluProAlaProThrThrThrLysSerAla	GCCCGCCGCCGCGCACCACCGAAGAGATCATCGAGGTGTGCCGGCCGCTGAGCG	sell	AGGAAGCCATGGCCAGCGGCGCCCATCGGCATTTCGACCGGCGCCTTCTACC	ro 4	ត ត	w	ရ	GluProAlaProThrThrProLysGluProThrProThrThrProLysGluProAlaPro

TELEPHONE: (61) INFORMATION FOR SEQ ID SEQUENCE CHARACTER LENGTH: 1314 TYPE: amino a MOLECULE TYPE: pro SEQUENCE DESCRIPTI 10-124-557-50
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971 CCGAACTGAGCGGGCGCGACCTTGAAAGCGGCGCACCTGAACAGCGCGAACTGAACACCAACTGAACCGAACTGAACCGAACCTGAACCGAACCTGAACCCGAACCTGAACCACGAACCTGAACCCGAACCTGAACCACGAACCTGAACCACGAACCTGAACCACGAACCTGAACCACGAACCATGAATCGAACCATGAATCGAACCACGAACCATGAATCGAACCATGAATCGAACCATGAATCGAACCACGAACCATGAATCGAACACCATGAATCGAACACCATGAATCGAACACTGAACACCATGAATCAACACGAACATGAATCAACACGAACATGAATCAACACGAACATGAATCAACACGAACATGAATCAACACGAACATGAATCAACACGAACATGAATCAACACGAACATGAATCAACACGAACAACAACAACAACAACAACAACAACAACAAC
GRATGANGTCGCGGCCGAGCCGGCAAATCCAAATCCAAATCCAAGTACG COLYSLYSLeuThrProThrThrProGluLySLeuAla GCCGGCCCATCTACTTCATGATGAACGAACCCGACG CITHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

Search completed: May 11, 2003, 12:30:20 Job time : 96.5 secs

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Result
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Listing first 45 summaries
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"OP-C972_1/USP70_spool/US1009782/runat_07052003_122518_23179/app_query.fasta_1.1927

-DB-Issued_Patents_AA -OFMT-fastan -SUFFIX-rai -MinmArCH-0.1 -LOOPCI-0

-LOOPEXT-0 -UNITS-bits -START=1 -END--1 -MATRIX-blosum62 -TRANS-human40 cdi

-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 cdi

-MILST-45 -DOCALIGN-200 -TORM-ext -HEARSES-500 -MINLEN-0 -MAXLEN-200000000

-USER-US10009782_eCGN 1_1_21_erunat_07052103_122518_23179 -NCPU-6 -ICPU-3

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ALIGNMENTS

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Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity:	RESULT 1 US-09-413-814-79 US-09-413-814-79 US-09-413-814-79 US-09-413-814-79 Sequence 79, Application US/09413814 Patent No. 6225064 GENERAL INFORMATION: APPLICANT: Bristol-Myers Squibb, Co. APPLICANT: Bristol-Myers Steven L APPLICANT: Bougherty, Brian A APPLICANT: Mueller, Joachim APPLICANT: Mueller, Joachim APPLICANT: Reichebach, Hans APPLICANT: Reichebach, Hans ITITLE OF INVENTION: DNA sequences for enzymati ITITLE OF INVENTION: DNA sequences for enzymati ITITLE OF INVENTION: DNA sequences for enzymati ITITLE OF INVENTION: NUMBER: US/09/413,814 CURRENT APPLICATION NUMBER: US/09/413,814 CURRENT FILING DATE: 1998-10-09 EARLIER APPLICATION WUMBER: DE 198 46 493.2 NUMBER OF SEQ ID NOS: 107 EARLIER FILING DATE: 1998-10-09 NUMBER OF SEQ ID NOS: 107 SOFTWARE: Patentin Ver. 2.1 LENGTH: 1213 TYPE: PRT ORGANISM: Sorangium cellulosum US-09-413-814-79
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	etide or	APPLICANT: Brandt, Petra APPLICANT: Cino, Paul M APPLICANT: Dougherty, Brian A APPLICANT: Goldberg, Steven L APPLICANT: Goldberg, Steven L APPLICANT: Hofle, Gerhard APPLICANT: Mueller, Joachim APPLICANT: Reichenbach, Hans ITTLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide FILE REFERENCE: PCT/US 99/23535 CURRENT APPLICATION NUMBER: US/09/413,814 CURRENT FILING DATE: 1999-10-07 EARLIER APPLICATION NUMBER: DE 198 46 493.2 NUMBER OF SEQ ID NOS: 107 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 78 LENGTH: 882 TYPE: PRT ORGANISM: Sorangium cellulosum S-09-413-814-78	APP	

1498 CAGCCCTTACAATCCGGCGTGAACGGGGGGGGGGGGGGG	Qy
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392ProArgArgPro-ArgAspArgArgProArgArgLeuLeuA	Db

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CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 277
LENGTH: 558
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-277
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Cao, Hui
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Goodman, Howard M.
Rahme, Laurence G.
Mahajan-Miklos, Shalina
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           Bloecker, Helmut
Brandt, Petra
Cino, Paul M
Dougherty, Brian A
Goldberg, Steven L
Hofle, Gerhard
Mueller, Joachim
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Beyer, Stefan
Reichenbach,
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US-09-413-814-79
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CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
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216 AlaArgAlaGlyAspArgValGluLeuGlyProGlyAlaAspGlyAspAlaHisGlyArg 235
                                                            196 ArgArgAspProArgProTyrProArgLeuGlySerGlyAlaLeuAlaArgAlaArgGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -------AGGGAGGGGCCATGTAGCGGTTTGCGTCCAGGGTTG 1544
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Matches:
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ESULT 7 Sequence 14, Patent No. 64 GENERAL INFO GENERAL OF 11 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: CORRESPOND! ADDRESSEE CITY: CE STATE: NO. COUNTRY: ZIP: O21 COMPUTER RE MEDIUM TY COMPUTER RE MEDIUM TY COMPUTER: OPERATING SOFTMARE: OPERATING DAN CLASSIFIC. PRIOR APPLICATI	1726 778	1686 758	738	718 1642	701 1603	5 68 4 45	66 48	647 1435	627	617 1328	1268
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N 7) NOTE: 14 APPLICANT: G. PPLICANT: G. PPLICANT: G. PPLICANT: H. PPLICANT: MASS. STREET: MASS. COUNTR: Cambistant: Countra: Mass. COUNTR: Cambistant: Countra: U. ZIP: Cambistant: U. ZIP: Cambistant: PPLICANTING SY. SOFTMARE: P. CAMPUTER TYPE: COMPUTER TYPE: COMPUTER TYPE: COMPUTER TYPE: CONTRARE: P. PPLICATION DATE: CARSIFICATION DATE: CLASSIFICATION DATE: IOR APPLICATION DATE: IOR APPLIC	АТБ ПП В	61A	ξĵ	Pro	TA:	or de	Asp	2 7 C	Sej	ଦ୍	G
PATT 7 7-7-7-022B-14 PINCORE 14, APPLICATION: APPLICANT: Gesner, APPLICANT: Clark, APPLICANT: Clark, APPLICANT: Hewick, TITLE OF INVENTION: APPLICANT: HEWICK, TITLE OF INVENTION: APPLICAT: Hewick, TITLE OF INVENTION: APPLICATION CAMBE STATE: MASSACHUS STATE: MASSACHUS COUNTRY: U.S.A. ZIP: 02140 COMPUTER READABLE FOR MEDIUM TYPE: Floy OPERATING SYSTEM: SOFTMARE: PATENTION NUMBER FILLING DATE: 1991 CLASSIFICATION DA APPLICATION NUMBER FILLING DATE: 18-0 RIOR APPLICATION NUMBER	CTGGGCCA aGlyPro	Pro	<u>`</u> }=	ece orași	roProGly GATATCGTGGG-	Pro-	C P	61 13 60 60 60 60 60 60 60 60 60 60 60 60 60	₹=	TGTTCGA	GCI
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tion US/0775: Thomas G. Stephen C. Stephen C. Katherine		yPr	YPz	E H			opr - de	. 61 - 62 - 63	8	ProGly	- ii
Thomas G. Stephen C. Katherine Rodney M. Megakarye: 143 ESS: 16S Instituting Park Dr idgePark Dr etts PPY disk compatible compatible PC-DOS/MS DATA: 10S 07/6. AN-1991 TA: US 07/54		65 :	. §−6	6 6	÷ + 5		ရှိ ရုံ	y≱_ 660	·γPι	- Y	- g
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Best Local Similarity:
Query Match:
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Pred. No.:
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INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
614 CGCCCGCCGCCCCCCCA---CCACCGAAGAGATCATCGAGGTGTGCCGGCCGCTGAGCG 670
                                     294 ThrThrProLysGluProAlaProThrThrProLys-----GluProAlaProThrThr 311
                                                             554 ACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCATCGGCATTTCGACCGGCGCCTTCTACC 613
                                                                                                                                                                                             271 ThrThrLysGluProAlaProThrThrPro-----
                                                                                                                                                  494 CCGCGGTCATGCCGGACTTGCAGCGCGCCGCCACCGACGAGGAAATCGCGGGCCATGCGGG 553
                                                                                                                                                                                                                                                                 251 GluProAlaProThrThrProLysGluProThrProThrThrProLysGluProAlapro 270
                                                                                                                                                                                                                             443 CGCCGGCGG------CCGTCAACGCCGCCTGTATGGTGGGCCATTCAACGCTGCGCG 493
                                                                                                                                                                                                                                                                                                      383 ACGAAGGCGGCTCTTACCGTTTCGAGCGCTTCGCCGACTACCTGGACGCGTTGCGGGCCA 442
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               229 AlaProThrThr---
                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 GGCGTCGCGACATGACGCCCAAGATCTCGCAGGGCGTCACCACGGTGGTCACGGGCAATT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 GCCTGGTGGTCGCCCCGGCTTCATCGACTCGCACACCACGACGACGACTACCTGCTCA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 ProThrProThrThrIleLysSerAlaProThrThrProLysGluProAlaProThrThr 186
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 -------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 GCATCGCCGCCATCGGCGATCTGTCGGACGCCGCGCACACCCCGGGTCGACGTGTCGG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 ThrLysSerAlaProThrThrProLysGluProAlaProThr---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 CCATGTCCCAATCCGATTCCCAGCCCTTCGACCTGCTGCTCGCGGGGGGGCACCCTCATCG 91
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29-DEC-1989
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Matches:
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Indels:
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5 AGGCCAGCGGCATCGCGGTCTCGACCCTGTCCAAGGCCGAGCTGGGCC 1732		Qy
2LysGluProAlaProThrThrProLysGlyThrAlaProThrThrLeuLys	572	В
	1625 TG	Qγ
ThrThrProLysGluProAlaProThrThrPro	561	D 4
6ThrSerAspLysbroAlabroThrThrProLysGlyThrAlaPro		ę b
TACAATCCGGCGTGAACGGGGGGGGGGGGGGGGGGGGGG	05	Q
ProAlaProLysGluLeuAlaProThrThrThrLysGluProThrSerThr 5	529 Pı	₽
CCGGCCAGCATGCCGGCCGCGTGCTCGCACGCCACGGCCTGAGCCCGGCCGCCGCCAGCCCCCCCC	1445 C	ο γ
	510 P	Db.
CCGCCGGCATCCATTCCGTGTACGTCAACGGCGCGCCGGTCTGGCAAGAGCAAGAGCTTTCA	1385 C	νQ
AlaProThrThrProLysGluProAlaProThrThrProLysGluThrAlaProThrThr	490 A	밁
8 TGTTCGACCCGGCCACGGTGGCCGATACCGCCACCTTCGAACACCCTACCGAGACACCCT	ы	Qy
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8 CGCGCTTCGGCCTGGCCGGGCGGCAGCTGCAGGCCGGGTACTTCGCCGACCTGGTGG 13		· Ωγ
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GCGACCTGGGCCTGTTCCCCGCTGGAGACGGCGGTATGGAAGATGACCGGCCTGACCGCCG 12	1208 G	Q
9	469 -	рь
8 ACCAGCGCCCCCATCCGCGCCTGTGGGGCACCTTCCCCGCGGGTGCTGGGGGCACTATGCGC 12		Qy
	453 T	ф
TGCAGCGCATCCTGGCCTTCGGCCCGACCATGATCGGCTCCGACGGCCTGCCGCACG 11	T. 1601	Qy
ProThrThrProGluLysProAlaProThrThrProGluGluLeuAlaProThr 452	435 P	Дb
ACGIGGIGCCCGAGCIGCAGCCGGCCGCCCATCIACTICATGAIGGACGAACCCGACG 1	4 1031	γQ
LysGluThrAlaProThrThrProLysLysLeuThrProThrThrProGluLysLeuAla	415 I	Дb
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95 ProThrThrThrLysLysProAlaProThrAlaProLysGluProAlaProThrThrPro		Db
11 TCAAGCAGGACCGCGTGCTGCTGGCCGGACGCACCATCATCACCTGGTGCAAGCCCTTCC 97		Qy
75 LysLysProAlaProThrThrProLysGluProAlaProThrThrProLysGluProAla	σ,	дg
51 CCATGGCGCGCCAGGACGTCTCGCTGGACGCGTATCCCTACGTGGCCGGCTCCACCATGC 91		Qy
66 ProLysGluProAlaPro	σ	Д
91 AGGTCATGGGCCAGCCCAATTTCGGCCGCTCGCGCGAGACGCTGCCGCTGATCGAGGCCG 8	1	γQ
		Дb
31 TGGAGGAAACCTTCCGCATCGGCCGCGAGCTGGACGTGCCGGTGGTGATCTCGCACCACA 79		, VQ
ProThrThrTysGluProAlaProThrThrTysSerAlaProThrThrProLvs 3	332.1	Db.
71 CGCATGGCGGCATCTACGCCACCCACATGCGCGACGAAGGCGAGCACATCGTGGCCGCGC		VQ
312 ThrLysGluProSerProThrThrProLysGluProAlaProThrThrThrLysSerAla 331		타

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US-10-009-782-1 (1-1758) x US-07-757-022B-84 (1-1022)
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Best Local Similarity:
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US-07-757-022B-84
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                                                                                                                                                                                                No.:
                                                                                                                                                                                                                                                        TOPOLOGY: 15
                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1022 amino aci
      248 ProThrProThrThrIleLysSerAlaProThrThrProLysGluProAlaProThrThr 267
                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: GI
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                                                                                                                                                                                                                                                                                       AMINO ACID
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Matches:
Conservative:
Mismatches:
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534 ThrProGluGluProThrProThrThrProGluGluProAlaProThrThr---
                                                                                                                                               971 CCGAACTGAGCGGGGGGGGACCTGGATGAAGTCGCGGGCGAGCGGGGAAATCCAAGTACG 1030
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                                                                                                                  LysGluThrAlaproThrThrProLysLysLeuThrProThrThrProGluLysLeuAla 515
                                                                                                                                                                                                             TCAAGCAGGACCGCGTGCTGCTGGCCGGACGCACCATCATCACCTGGTGCAAGCCCTTCC
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                                                        ---GluLysProAlaProThrThrProGluGluLeuAlaProThr
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ACGAGCGCCCGCATCCGCGCCTGTGGGGCACCTTCCCGCGGGTGCTGGGGGCACTATGCGC 1207

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COMPUTER: IBM PC COMPANY DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1625 TGGGCGCGCGCCTGCGCGCGCGAGCGCAAGGCCCGGAAAATGACCCTGCAAGACCTGTCGC 168
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                                                                                                                                                                                                                                                                                                                                                                     Megakaryocyte Stimulating Factors
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 494
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NAME: Cserr, Luann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 18-JAN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 CCATGTCCCAATCCGATTCCCAGCCCTTCGACCTGCTGCTCGCGGGGGGGCACCCTCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELECOMMUNICATION INFORMATION: TELEPHONE: (617)876-1170
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REFERENCE/DOCKET NUMBER: GI
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                                                                                           CCGCGGTCATGCCGGACTTGCAGCGCGCCGCCCACCGACGAAAATCGCGGCCATGCGGG 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCTGGTGGTCGCCCCGGCTTCATCGACTCGCACACCACGACGACAACTACCTGCTCA 262
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08-AUG-1989
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29-DEC-1989
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                                                                                                                                                                        -----CCGTCAACGCCGCCTGTATGGTGGGCCATTCAACGCTGCGCG 493
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                                                                                                                                                                                                                                                                                      -ThrThrProLysLysProAlaProThrThrProLys 315
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Indels:
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US-07-757-022B-74

1733 AGATCGCCCTGAGCTACGAGAAGC 1756

690 LysGlyProThrSerThrThrSer 697

1685

653

Sequence 74, Application US/07757022B Patent No. 6433142

INFORMATION:

TITLE OF INVENTION: MUMBER OF SEQUENCES:
ORRESPONDENCE ADDRESS

ADDRESSEE:

3: Genetics Institute, 87 CambridgePark Drive

Inc.

PPLICANT: Gesner, Thomas G.
PPLICANT: Clark, Stephen C.
PPLICANT: Turner, Katherine
PPLICANT: Hewick, Rodney M.

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS

COUNTRY: U ZIP: 02140

U.S.A.

CITY: Cambridge STATE: Massachusetts

APPLICATION NUMBER:

US 07/643,502

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431 ProLysGluProAlaPro-----

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                                       1625 TGGGCGCGCGCGCGCGCGAGCGCAAGGCCCGGAAAATGACCCTGCAAGACCTGTCGC 1684
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                                                                                                                                                                                                                                                                                                      575 ProLysGlyThrAlaPro---ThrThrLeuLysGluProAlaProThrThrProLysLys 593
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   -----LysGluProAlaProThrThrProLysGlyThrAlaPro---ThrThrLeuLys 653
                                                                                                                                                                                                                                                                   CCGGCCAGCATGCCGGCCGCGTGCTCGCACGCACGGCCGCCTGAGCCCGGCGCCAGCCCT 1504
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US-10-009-782-1 (1-1758) x US-07-757-022B-58 (1-1049)
                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                            Alignment Scores: Pred. No.:
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US-07-757-022B-58
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                                                                                                                                                                                                   -757-022B-58
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                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CSEIT, LUANN
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                                                                                                                                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVERTION: Megakaryocyte Stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1733 AGATCGCCCTGAGCTACGAGAAGC 1756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Cambridge
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08-AUG-1989
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29-JUN-1990
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) v	543 ProThrThrProGluLysProAlaProThrThrProGluGluLeuAlaProThr 560	
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	NUMBER OF ENVENIEUR: MEGARATYOCYTE STIMULATING FACTORS CORRESPONDENCE ADDRESS:	88:	
	T: Hewick, Rodney M. Trurphmrov, Rodney M.	AP	
	Gesner, Clark, S	AP AP	
•	ce 104, Applicati No. 6433142 AL INFORMATION:	; Sequence ; Patent No ; GENERAL	
	022B	RESULT 11 US-07-757-	
	717 LysGlyProThrSerThrThrSer 724	Db 7	
	TCGCCCTGAGCTACGAGAAGC 1756	QY 17	
716	97 GluProAlaProThrThrProLysLysProAlaProLysGluLeuAla	Db 6	
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	579 LysAlaAlaAlaProAsnThrProLysGluProAlaProThrThrProLysGluPro	Дb	
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	GluProAla CGCCGGCGG ::: ThrThrLys	GCGG	GGCG	•	CCATG	ment Scores: No.: strict nt Similarity: Local Similarit Match:	CLASSIFICATION PRIOR APPLICATION PETLING DATE: PRIOR APPLICATION PETLING DATE: PRIOR APPLICATION NOTICE PRIOR APPLICATION NOTICE PRIOR APPLICATION NOTICE PRIOR APPLICATION NOTICE COMMUNICATION NAME: CSETT REGISTRATION NAME: CSETT REFERENCE/DOCUMENT PRIOR APPLICATION NAME: CSETT REFERENCE/DOCUMENT OF COMMUNICATION REFERENCE/DOCUMENT OF CASACTION NAME: CSETT RELEPHONE: (61 TELEPHONE: 1140 TYPE: AMINO TYPE: AMINO TYPE: AMINO TYPE: AMINO TYPE: AMINO TYPE: AMINO TYPE: 1140 TYPE: 1100 TOPOLOGY: 1140 TYPE: 1100 TOPOLOGY: 1140 TYPE: MOLECULE TYPE:
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CAGCO	COLYSC COTCAL COTAL	GCTGG	CAAGA	ACACCCGG	S-07-	**************************************	I: 530 II: 530 III: 530 IIII: 530 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
AGCGCGCCGCCA LysGluProAla	3luPro	CGCAC	TCTCG TCTCG TCTCG TCTCG	CGGAC	757-0: CCCTT		/546 /546 /546 /390 /390 /390 /390 /390
CCACC	SCCIG	ACGCCAA hrProL	TCGCA ::: rLysG CAGGG : sGlup	GCCGC	022B-104 TCGACCTG ProThrTh	Length: Matches: Conservat M1smatche Indels: Gaps:	13,502 16,114 17,196 0,901 5190
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GAGGAAATCGCGGCCA 	uThrProLysGluPro	CGCACGCCAACCCGCCCCCCCTGGACC ThrThrProLysLysProAlaProThrThr AGCGCTTCGCCGACTACCTGGACGCGTTGC	CCACGACGACAACTACC	CCGACCTGGGCGTGCGCC	(1-1140) TGCTCGCGGGCGGCACCO ProLysGluProAlaPro	114 137 1ve: 60 s: 240	
GCGGTCATGCCGGACTTGCAGCGGCGCCACCGACGAGGAAATCGCGGCCATGCGGC 	GluproAlaProThrThrProLysGluProThrProThrThrProLysGluProAlaPr. CGCCGGCGGCCGTCAACGCCGCCTGTATGGTGGGCCATTCAACGCTGCGC.	GCCCGCCCCCTGGACCTGCTG::	CCACGACGACAACTACCTGCTC roalaproThrThrThrLysse caccacggggar :: ::	GGGCGGCGCCGACCTGGGCGTGCGGCGAC "SGluProAlaProThrT) GACGCCGCCGCACACCCGGGTCGACGTGTCG "ThrThrProLysGluProAlaProThr	(1-1140) TGCTCGCGGGCGCGCCCTCATO ::: ProLysGluProAlaProThrT)	114 137 1ve: 60 s: 240	
CCGACGAGGAAATCGCGGCCATGCGGG 553 	rProLysGluProThrProThrThrProLysGluProAlaPro 469 -CCGTCAACGCCGCCTGTATGGTGGGCCATTCAACGCTGCGCG 493 :::	ପ୍ରତ୍ର	ACGACAACTACCTGCTCA	ThriysGluProAlaproThrihrProLysGluProAlaProThr 415 ThriysGluProAlaProThr	782-1 (1-1758) x US-07-757-0228-104 (1-1140) CCATGTCCCAATCCGATTCCCAGCCCTTCGACCTGCTGCTGCTGCGGGGGGGACCCTCATCG 91	114 137 1ve: 60 s: 240	

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Percent Similarity:
Best Local Similarity:
                                Query Match:
                                                                                                                        Alignment Scores:
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US-07-757-022B-44
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                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 40
SEQUENCE CHARACTERISTICS:
LENGTH: 1270 amino acids
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                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,02:
FILLING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 29-DEC-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 29-JUN-1990
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                            TTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLE OF
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87 CambridgePark Drive
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                                                                                                                                                                                                                                                                                           (617)
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29-DEC-1989
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Matches:
Conservative:
Mismatches:
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1031 ACGTGGTGCCCGAGCTGCAGCCGGCCGCCGCCATCTACTTCATGATGGACGAACCCGACG 1090
                                                                                                                          460
                                    480 LysGluThrAlaProThrThrProLysLysLeuThrProThrThrProGluLysLeuAla 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 GGCGTCGCGACATGACGCCCAAGATCTCGCAGGGCGTCACCACGGTGGTCACGGGCAATT
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                                                                                                            ProThrThrThrLysLysProAlaProThrAlaProLysGluProAlaProThrThrPro
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553 345 335

303 322 293 262 202

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281

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850

430 790

416 730 396 670 376 613

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Patent No. 6433142

GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryoc;
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSES:
                                                                                                                                                                                                                                                                                                                                                                Sequence 42, Application US/07757022B Patent No. 6433142
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1685 AGGCCAGCG---GCATCGCGGTCTCGACCCTGTCCAAGG------CCGAGCTGGGCC 1732
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                                                                                                                                  CITY: Cambridge
STATE: Massachusetts
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                                                                                                                                                               87 CambridgePark Drive
   PatentIn Release #1.0,
                                                                                                                                                                                     Genetics Institute, Inc
                                                                                                                                                                                                                                        Megakaryocyte Stimulating Factors
Version #1.25
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TELEPAX: (617)876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 amino act
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TELEPHONE: (617)876-5851
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APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
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REGISTRATION NUMBER: 31,822
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RESULT 13 US-07-757-022B-42

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7.01e- 285.50 33.50%	B76 876 B76 B76 B76 B76 B76 B76 B76 B76 B76 B	APPLICATION DATA: LICATION NUMBER: US 07/457,196 APPLICATION DATA: LICATION DATA: LICATION DATA: LICATION NUMBER: US 07/390,901 ING DATE: 08-AUG-1989 ING DATE: 08-AUG-1989 ING DATE: 08-AUG-1989 ING DATE: 08-AUG-1989 ING DATE: 108-AUG-1989 ING DATE: 108-AUG-1989 ING DATE: 08-AUG-1989 ING DATE: 08-AUG-1989 ING DATE: 1989 ING DATE: 1989 ING DATE: 1989 ING DATE: 1989 ING DATE: 1990	CURRENT APPLICATION DATA; APPLICATION NUMBER: US/07/ FILING DATE: 19910910 CLASSIFICATION DATA; PRIOR APPLICATION DATA; APPLICATION UNMBER: US 07/ EILING DATE: 18-JAN-1991 PRIOR APPLICATION UMBER: US 07/ EILING DATE: US 07/ EILING DATE: US 07/ EILING APPLICATION NUMBER: US 07/ EILING DATE: US 07/	1	42 Application 3142 Gesner, Th Clark, Stej Furner, Kaj Hewick, Ro VENTION: MA EQUENCES:	ThrihrprolysGluproAlapro TGGGCGCGCGCGCGCGGCGGCGGCCGAGC ::: :::LysGluproAlaproThr AGGCCAGCGGCATCGCGGTCT GluproAlaproThrihrproLys AGATCGCCCTGAGCTACGAGAAGC ::: LysGluproThrSerThrSerThrSer	_
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CG 109 CG 114 CG 114 CG 114 CG 120 CG 120 CG 120 CG 132; CO 597 CO 597 CO 597 CO 1384 CF 617 CF 653 CF 1564 CF 17 1564	SULT 15 -07-757-022B-50 -07-757-022B-50 Sequence 50, Application US/07757022B Patent No. 6433142 GENERAL INFORMATION: APPLICANT: Gesner, Thomas G. APPLICANT: Gesner, Katherine APPLICANT: Hewick, Rodney M. TITLE OF INVENTION: Megakaryocyte Stimulating NUMBER OF SEQUENCES: 143 CORRESPONDENCE ADDRESS: ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02140 COMPUTER READABLE FORM: MEDDIUM TYPE: Floppy disk	1733 AGATICGCCCTGAGCTACGAGAAGC ::: ::: 717 LysGlyProThrSerThrThrSer	697 GluproAlaproThrThrproLysLysproAlaproLysGluLeuAlaproThrThrThr	1923 TEGEOGGECCTGCGCGCCGACGCAAGGCCCGGAAAATGACCCTGCAAGACCTGTCGC ::: ::: 680LysGluproAlaProThrThrProLysGlyThrAlaProThrThrLeuLys	1993 ACATGGCCCCTCCCCTCCGCTCGCAATACGGCCCCACCCGATÄTCGTGGGCAAGGAAGTGA	654ThrSerAspLysproAlaproThrProLysGlyThrAlapro	149 CUGUCAGCATGCGGCGCGCGTGCTGCACGCACGCCCTGAGCCCGGCGGCCACGCCCT	. 1445	1328 598	579	578	1208	577	561	1091 TGCAGCGCATCCTGGCG	1031 ACGTGGTGCCCGAGCTG 543 ProThrThrPro

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US-10-009-782-1 (1-1758) x US-07-757-022B-50 (1-1314)
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1314 amino aci
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION UNMBER: US 07/546,114
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
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RIOR APPLICATION DATA:
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28-DEC-2000.	WO200078926-A1.	Alcaligenes xylosoxidans.	D-aminoacylase; zinc tolerant host; recombinant production; zinc-enhanced expression; D-form amino acid synthesis; antibiotic production; peptide drug; pharmaceutical manufacturing.	Alcaligenes xylosoxidans subspecies xylosoxidans D-aminoacylase.	27-MAR-2001 (first entry)	AAB48975;	AAB48975 standard; Protein; 484 AA.	RESULT 1.

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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a recombinant zinc-tolerant microorganism which expresses the D-aminoacylase from Alcaligenes xylosoxidans subspecies xylosoxidans. The presence of zinc ions in the culture medium enhances the process of recombinantly producing the D-aminoacylase to microorganism of the invention also relates to microorganism of the invention. The recombinant microorganism is used synthesis of high optical-purity D-form amino acids for use ful in the production of antibiotics and peptide drugs. The present sequence represents Alcaligenes xylosoxidans subspecies xylosoxidans
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                                                                                                                            81 MetThrProLysileSerGlnGlyValThrThrValValThrGlyAsnCysGlyileSer
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GTCAACGCCGCCTGTATGGTGGGCCATTCAACGCTGCGCGCCGCGGGTCATGCCGGACTTG
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                                                                                                                                                                                                                                                                             The present sequence represents an aminocyclase enzyme. The enzyme capable of hydrolysing N-acetyl-D-tryptophan at a substrate concentration of 10 grams per litre, and exhibiting faster converse of R-N-acetyl-2-thienylalanine than of R-N-acetyl-4-chlorophenylalanine. The enzyme can be used for the preparation of a D-amino acid by conversion of a corresponding D-N-acylamino acid. It can also be used for resolving a racemic mixture of N-acylamino acids and deprotecting optically-enriched the production of various pesticides, antibiotics and other harmananticals.
                                                                                                                                                                                                                                                                                                                                                                                                          New isolated D-amino acylase enzyme, useful for the preparation D-amino acids for use as intermediates in the preparation of pesticides, antibiotics and other pharmaceuticals
                                                                                                                                                                                                                                                                         pharmaceuticals.
                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 20-22;
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                                                                                                                                                       The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi i a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to lid degrees centigrade.

110 degrees centigrade.

Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                      Claim 7; Pages 694-696; 1657pp; French
                                                                                                                                                                                                                                                                                            New nucleotide sequences isolated proteins useful in industry -
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                                  GACCTGGATGAAGTCGCGGCCAGCGCGCAAATCCAAGTACGACGTGGTGCCCGAGCTG
                                                                                                        GCCGGA-----CGCACCATCATCACCTGGTGCAAGCCCTTCCCCGAACTGAGCGGGCGC
SerLeuLysGluIleSerAspLeuLeuH1sArgAspProPheAspValLeuPheAspIle
                                                                    AlaGlyTrpGluAsnIleIleThrHisSerGluAsnPheProGluPheValGlyLys
                                                                                                                                              ArgLysLysIleArgGluPheIleGluThrArgAspAspTrpGlnAsnPheIleLysGlu
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                                                                                                                                                                                                                                                                                                                               ---GACGTCTCGCTGGACGCGTATCCCTACGTGGCCGGCTCCACCATGCTCAAG-----
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                                                                                                                                                                                  ----CAGGACCGCGTGCTGCTG
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                                               Novel D-aminoacylase-encoding gene derived Hypomyces mycophilus, useful for producing N-acetyl-D-tryptophan, useful as medicinal
   This sequence
                           Claim 1; Page 17-20; 33pp; English.
                                                                                                                                          Mitsuhashi K,
                                                                                                                                                                                                                                                                                                                     D-aminoacylase; N-acetyl-D-tryptophan; N-acetyl-D-phenylalanine; PCR; N-acetyl-D-valine; N-acetyl-D-leucine; N-acetyl-D-methionine; primer; probe; synthesis; detection; D-amino acid; substrate specific; amplify; thermal stability; polymerase chain reaction.
                                                                                                                                                                (DAIL ) DAICEL CHEM IND LTD
                                                                                                                                                                                         27-JAN-2000;
22-MAY-2000;
                                                                                                                                                                                                                            25-JAN-2001; 2001EP-0101739
                                                                                                                                                                                                                                                       01-AUG-2001
                                                                                                                                                                                                                                                                                                       Hypomyces mycophilus.
                                                                                                                                                                                                                                                                                                                                                                                          D-aminoacylase.
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DB; AAH43261.
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                                                                                                                                                                                        2000JP-0019080
2000JP-0150578
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
   shows a D-aminoacylase
                                                                                                                                        Yamamoto H,
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                                                                                                                                     Tokuyama
                                                 from filamentous fungus
D-tryptophan from
raw material -
D-aminoacylase
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
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          204
                                                                         184
                                                                                                         538
                                                                                                                                          164
                                                                                                                                                                          478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-acetyl-D-amino acids to produce the corresponding D-amino acids, and substrate specificity, where the enzyme acts on N-acetyl-D-tryptophan, N-acetyl-D-phenylalanine, N-acetyl-D-valine, N-acetyl-D-nethionine, but not on
                                                                                                                                                                                                         144
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                                                                                                                                                                                                                                                                          124
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                                                                                                                                                                                                                                                                                                                               104 AsnValAspGinLeuArgAlaIleArgGluGlnIleAlaGlyTrpAsnGlyAsnProThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               low cost and in large quantities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GluIleLeuPheHisSerAlaThrValIleThrGlyAspGluAlaAlaGlnProPheVal
SerGlyLeuThrTyrThrProGlyMetTyrAlaSerThrSerGluLeuAlaSerLeuCys
                              ACCGGCGCCTTCTACCCGCGCGCGCGCGCGCGCACCAAGAGAGATCATCGAGGTGTGC
                                                                                                 ATCGCGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCCATCGGCATTTCG
                                                                                                                                GlnGlyAsnLeuArgLeuLeuAlaCysGlyProTyrAspThrProAlaSerAlaGluGlu
                                                                                                                                                                                               GluTyrLeuAspCysLeuGluArgAsnArgThrAlaThrAsnValAlaMetLeuValPro
                                                                                                                                                                                                                               GACTACCTGGACGCGTTGCGGGCCACGCCGGCGGCGGCCGTCAACGCCGCCTGTATGGTGGGC
                                                               CATTCAACGCTGCGCGCGCGGTCATGCCGGACTTGCAGCGCGCCGCCACCGACGAGGAA
                                                                                                                                                                                                                                                              AspGluGluCysArgThrThrLeuLysGlyValGlyMetPheGluTrpGlnThrIleGly
                                                                                                                                                                                                                                                                                                GAC-----CTGCTGGACGAAGGCGGCTCTTACCGTTTCGAGCGCTTCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                   TCGCAGGGCGTCACCACCGGTGGTCACGGGCAATTGCGGCATCAGCCTGGCGCCGCTGGCG 348
                                                                                                                                                                                                                                                                                                                                                                      CACGCCAACCCG----
                                                                                                                                                                                                                                                                                                                                                                                             ThrGlnGlyCysThrThrGluValValGlyGlnAspGlyIleSerTyrAlaProIleArg 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspMetH1sAlaH1sSerAspLeuTyrLeuLeuSerH1sProAspH1sGluAlaLysIle
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Indels:
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Matches:
Conservative:
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                                                                   ThrLeuArgArgSer
                                                                                           GTGCTCGCACGCACG 1479
                                                                                                            LeuValAsnGlyGlnIleAlaValAspGluGlyLysMetThrGlyThrArgGlyGlyLys
                                                                                                                                  ValLysAspMetSerThrTyrGluGluProLysValProSerArgGlyIleArgPheVal
                                                                                                                                                                                                                                GGGCGCGGGCAGCTGCAGGCCGGGTACTTCGCCGACCTGGTGGTGTTCGACCCGGCCACG 1344
                                                                                                                                                                                                                                                      LeuProSerMetIleAlaHisLeuThrSerArgProAlaLysArgLeuSerValTyrPro 483
                                                                                                                                                                                                                                                                               HisArgValHisMetAlaGlySerAspGlyIleLeuHisGlyGlnThrLeuHisProArg
                                                                                                                                                                                                                                                                                                                                                                                                       \textbf{LeuAlaThrSerCysIleMetHisValGlyAsnGluGluAsnValArgGlnIleMetGln}
                                                                                                                                                                                                                                                                                                                                                                                                                               CAGCCGGCCGCCCATCTACTTCATGATGGACGAACCCGACGTGCAGCGCATCCTGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt IleGlyThrThrAsnGluProSerIleAlaSerTyrSerGlyArgArgLeuSerGluVal}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProGlnGluThrLeuLysArgLeuGluAspAlaGluSerArgGluLysIleArgIleAla 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TyrLeuProGlyCysThrThrLeuAlaAlaLeuLeuProSerTrpAlaSerAlaGlyGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt PheGlnAlaIleGluSerTyrAlaGluMetLeuAspLeuGlyGluSerThrGlyCysPro}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein; 1212 AA
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                                                                                                                                                                                                                                                                                                                 Pred.
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Creceptor subunit (NMDAR). The nucleic acid sequence does not contain
Ct the 366 5'-most nucleotides, by the insertion of 11 nucleotides between
Creceptor subunit (NMDAR). The nucleotides at positions
Creceptor subunit of 1301, nor the 15 nucleotides at positions
Creceptor subunit of NMDA-activated cation-selective ion channels. In
Creceptor subunit of NMDA-activated cation-selective ion channels. In
Creceptor subunit of the production of NMDA receptor subunit
Creceptor subunit of subunitate nucleic acids are also useful as probes to identify and
Creceptor subunit of subunitations of one type (homomeric) or from combinations of subunit proteins of one type (homomeric) or from combinations of subunit proteins of aliferent types (heteromeric). The present invention also comprises
Creceptor subunits to identify and characterise of different subunit affect the function of such receptors of a sponists,
Creceptor subunits to identify and characterise compounds which affect the function of such receptors of subunits to comprises methods for determining whether unknown protein(s) are
Creceptor subunits and modulators of glutamate receptor function. The invention comprises methods for determining whether unknown protein(s) are
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113 GGCGCGCG------ACCTGGGCGTGCGCGGCGACCGCATCGCCGCCATCGGCGATC 163
                                                                                                                  370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding N-methyl-D-aspartate receptor subunit - useful for the assembly of functional glutamate receptor subunits
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20-APR-1993;
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                                                                                56
                                                                                                                                              32 CCATGTCCC-------AATCCGATT----
                                                                   CCTTCGACCTGCTGCTGCGGGGGGGGCACCCTCATCGACGGCAGCAACACCCCGG----GGC
                                 ProSerSerAlaValArgAspSerAlaSerThrSerSerArgSerTrpProGluTrpSer 409
                                                                                                      ProCysProAlaAlaGlyArgAlaThrThrProSerAlaAlaGlyThrTrpProProThr 389
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                                                                                                                                                                                                                                                                                                                                                                 1212 AA;
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93US-0052449.
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 $\tt AsnSerProThrThrCysThrTrpProThrAlaSerMetAlaSerGlyCysAlaAlaTyr$

	JATGTNTATGALAALASerTrpThrSerThrThrTrpGluAlaSer 743	set stakt Ameryt		,
	CGTGGCCGGCTCCACCATGCTCAAGCAGG 91			<i>y</i> 4
	.YThrGluArgH1sArgAsnTr	ercysserser	JO	< 6
		GGACGTCT	70.0	. ⊷
	erProCysArgArgThrProThrGlySerGlyProThrTrpArg 7	roLeuA	000	Ō
	TGATCGAGGCCGCCATGGCGC 8		824	¥
	nAlaArgThrArgAlaAlaSerTrpSerProLeuGlyLeuAlaArgSerLeuLeu 683	pGlna	664	ŏ
	GGCCAGCCCAATTTCGGCCGCTCGCT	. ^	773	¥
	PG1ySerTrpMetProSerSerMetMetLeuLeuSerSerThrmh 663	::::::	644	ğ
	##SerThrSerAlaArgTrpArgThrArgSer	CTTCC	740	₹
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	::: erAlaValThrThr 6	LeuSer	Ö	8
	ATGGCGGCATCTACG 6		656	¥
	ysileSerThrHis 60	SerThr	585	B
	655	TCA	644	Ą
	SerSerProAspThrArgProThrTrpProProSerSerLysSerAsnThr 584	Ser	567	8
	CACCACCOCACOCACOCACOCACOCACOCACOCACOCAC	GCA	590	Ą
	laProProAlaArgSerTrpPheTrpSerGlyProSerLeuLeuSer 566	Arg	547	문
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	Throlnovabroser s	Leu	527	8
		1	548	δ
	:::::: AlaThrThrArgThrSerProGluAlaArgLeuSer 5	Суз	507	용
	CCGACGAGGAAATCGCGGCCA 5		503	γQ
	:::	4 LeuSerCysAlaSer	494	B
	CLOCOTOTATGGTGGGCCATTCAACGCTGCGCTATATGGCGCCCTGTATGTCGCCCATTCAACGCCTGTATGTTGTATGCTGCGCCATTCAACGCTGCTGTATGTTGTATGTTGTATGTTGTATGTA	3	44:	Ϋ́
		SerHisIleAlaLeu	48	B
	GTTTCGAGCGCTTCGCCGACTACCTGGACGCGTTCCCCCC	3 ACGAAGGCGGCT	38	δ
		7 Ala:	σ	B
	46	6 GCA:	N	γQ
0.	CACCACGGTGGTCACGGGCAATTG	4 6	4 <u>1</u>	문 5
•	roSerProSerMetArgAsn	dit.	n 4	5 5
0,	TGGTGGTCGCGCCCGGCTTCATCGACTCGCACCACCACGACGACAACTACCTGCTCAGGC 265	of Teer	20	3 5
~	:: InThr 4	0 стут	43	밁
OI .	TGTCGGACGCCGCGCGCACACCCCGGGTCGACGTGTCGGGCC 205	4	16	Ş

DXX DXX

23-FEB-1999 (first entry)

Human N-methyl-D-aspartate receptor subunit encoded by clone NMDA24.

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                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                      164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor subunit (NMDAR). The nucleic acid sequence does not contain 860 5'-most nucleotides, has an additional 11 nucleotides (AAV82891) between nucleotides 1300 and 1301, an additional 24 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a human N-methyl-D-aspartate receptor subunit (NMDAR). The nucleic acid sequence does not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding N-methyl-D-aspartate receptor subunit - assembly of functional glutamate receptor subunits
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N-PSDB; AAV82910.
         266
                                                                 246
                                                                                                113
                                                                                                                             226
                                                                                                                                                                          206 ProCysProAlaAlaGlyArgAlaThrThrProSerAlaAlaGlyThrTrpProProThr
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20-APR-1993;
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                                                                                                                                                        56
                                                                                                                                                                                                                 32 CCATGTCCC--
 GlyThrAlaLeuGlyArgCysThrThrSerGlyGlnThr---
                                                      {\tt AsnSerProThrThrCysThrTrpProThrAlaSerMetAlaSerGlyCysAlaAlaTyr}
                                                                                              GGCGCGCCG----
                                                                                                                 {\tt ProSerSerAlaValArgAspSerAlaSerThrSerSerArgSerTrpProGluTrpSer}
                                                                                                                                             CCTTCGACCTGCTGCTGCGGGGGGGGCACCCTCATCGACGGCAGCAACACCCCGG----GGC
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93US-0052449
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33.07%
25.17%
12.20%
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                                                                                   -- ACCTGGGCGTGCGCGCGACCGCATCGCCGATCGGCGATC
                          TGTCGGACGCCGCGCGCACACCCGGGTCGACGTGTCGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                     NMDA receptor subunits.
                                                                                                                                                                                                                                          (1-1061)
                                                                                                                                                                                                             -AATCCGATT-----
                                                                                                                                                                                                                                                                                                              Length:
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Best Local Similarity:
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Pred. No.:
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494 CCGCGGTCATGCCGGACTTGCAGCGGCGCCGCCGCCGACGAGGAAATCGCGGCCA-----
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                                                                 434 TGCGGGCCACGCCGGCGGCCGTCAACGCCGCCTGTATGGTGGGCCATTCAACGCTGCGCG 493
                                                                                                                  374 ACCTGCTGGACGAAGGCGGCTCTTACCGTTTCGAGCGCTTCGCCGACTACCTGGACGCGT 433
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                                                                                                                                                                                                                                                     449 -----TrpProSerAlaProSerProSerMetArgAsnAlaProArgSer***ThrSer 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a subunit (designated NMDARIA) of the human N-methyl-D-aspartate (NMDA) receptor. This is an ionotropic glutamate receptor which contains cation-specific ligand-gated ion channels. The protein and its coding sequence can be used in disease diagnosis and in research to identify other, similar proteins. They can also be used as probes, for example in genetic screening, and in drug screening, as well as enabling the production of animal disease models.
                                                                                                                                                                                                                                                                                                        434 TyrGlyThrAla***LeuGlyArgCysThrThrSerGlyGlnThr--------
                                                                                                                                                                                                                                                                              200 CGGGCCTGGTGGTCGCGCCCGGCTTCATCGACTCGC---ACACCCACGACGACGACTACC
                                                                                                                                                                                                                                                                                                                                                   140
                                                                                                                                                                                                                                                                                                                                                           414 AsnSerProThrThrCysThrTrp***ProThrAlaSerMetAlaSerGlyCysAlaAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel DNA fragment encoding human N-methyl-D-aspartate receptor subunit for identifying mutations and for developing drugs against various disease states
                                                                                                                                                                                                                                                                                                                                                                                                                                         56 CCTTCGACCTGCTGCTCGCGGGCGCCACCCTCATCGACGGCAGCAACACCCCGG----GGC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 CCATGTCCC------CCCAGC 55
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                                      CysGly---******CysLeuSerCysAlaSerLeuTrpTrpPro-----Ser 513
                                                                                          ProSerTrpSerHisIleAlaLeu-----Gln 498
                                                                                                                                             Leu-----TyrProLeuTrpArgArgAlaSerVal***Trp-----
                                                                                                                                                                                                                          TGCTCAGGCGTCGCGACATGACGCCCCAAGATCTCGCAGGGCGTCACCACGGTGGTCACGG 316
                                                                                                                                                                                                                                                                                                                                 GGCGCGCCG-----ACCTGG-------GCGTGCGCGCGCG 139
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DB; AAA95032.
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Db 514 ProSerSerCysSerSerThrEstrAlafeuSerAlafurthrAugthrSerProGluMla 531
514 ProSerSerCysSerSerThrSerThrSerProGluMla 548
4 ProSerSerCysSerSerThrSerAlafueuserAlafurThrArgThrSerProGluAla 8

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Novel nucleic acid encoding human N-methyl D-aspartate receptor
                                        WPI; 2002-096550/13
N-PSDB; ABI99189.
                                                                                      Daggett LP,
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20-APR-1993;
                                                                                                                                                                                                                            13-NOV-2001
                                                                                                                                                                                                                                                        US6316611-B1
                                                                                                                                                                                                                                                                                                                      Human; N-methyl D-aspartate receptor; NMDAR; genetic
glutamate receptor; drug; modulator; receptor
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                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              Human NMDA receptor subunit
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                                                                                      Lu C;
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93US-0052449.
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                                                                                                                                                                                                                                                                                                                 drug; modulator;
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Sequence

1232 AA;

of NMDAR

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cc nucleic acids are useful for the production of MMDAR subunits. The proteins (ABB5503-ABB5630, AAM47961), as probes and to identify and close the proteins (ABB5503-ABB5630, AAM47961), as probes and to identify and close the proteins (ABB5503-ABB5630, AAM47961), as probes and to identify and close to consider the proteins of the construction can be carried out using the nucleotide sequences as probes to consider the proteins of the construction can be considered to glutamate receptor systemation can be screened to determine if they are also predisposed to such disease states. Construction can be screened to determine if they are also predisposed to such disease states. Construction comprising (I) are useful for producing selected AMDAR construction subunits and in specific combinations, as well as antibodies to the receptor subunits substantially free of contamination from many other receptor proteins whose presence can interfere with analysis of a single observation of the effect of a drug substance on a particular receptor subtype or combination of MMAR subtypes allows the subtype or combination of MMAR subt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subunit, useful for expressing the subunit and as probes in genetic screening techniques, to identify patients having neuropathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to nucleic acids (I, AAI99167-AAI99196, ABA05910)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Column 257-264; 206pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding human N-methyl D-aspartate receptor
                                                           of drugs or modulators in a test system that human NMDAR subtype or the combination of NMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NMDAR) subunits.
                                                                                                    is specific for
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Ş 밁 Š Š 맑 밁 Š 멹 Š 밁 Ş 밁 S 밁 Š 밁 Š US-10-009-782-1 (1-1758) x AAM47961 (1-1232) Query Match: Percent Similarity: Best Local Similarity: Pred. No.: Alignment Scores: Score 434 TGCGGGCCACGCCGGCGGCCGTCAACGCCGCCTGTATGGTGGGCCATTCAACGCTGCGCGG 490 467 257 449 200 434 140 414 394 ProSerSerAlaValArgAspSerAlaSerThrSerSerArgSerTrpProGluTrpSer 374 ProCysProAlaAlaGlyArgAlaThrThrProSerAlaAlaGlyThrTrpProProThr 113 GGCGCGCCG------ACCTGG-----56 CCTTCGACCTGCTGCTGCGGGGGGCACCCTCATCGACGGCAGCAACACCCCGG---GGC 112 32 CCATGTCCC------AATCCGATT--ProSerTrpSerHisIleAlaLeu-----ACCTGCTGGACGAAGGCGGCTCTTACCGTTTCGAGCGCTTCGCCGACTACCTGGACGCGT TGCTCAGGCGTCGCGACATGACGCCCAAGATCTCGCAGGGCGTCACCACGGTGGTCACGG -----TrpProSerAlaProSerProSerMetArgAsnAlaProArgSer***ThrSer 466 CGGGCCTGGTGGTCGCCCCGGCTTCATCGACTCGC---ACACCCACGACGACAACTACC TyrGlyThrAla***LeuGlyArgCysThrThrSerGlyGlnThr---ACCGCATCGCCGTCGGCGATCTGTCGGACGCCGCGCGCACACCCGGGGTCGACGTGT 199 AsnSerProThrThrCysThrTrp***ProThrAlaSerMetAlaSerGlyCysAlaAla -----TyrProLeuTrpArgAlaSerVal***Trp-----5.32e-19 378.50 33.15% 25.37% 11.47% TrpLeuAlaAlaMetAlaProSerProProArg Length: Matches: Conservative: Gaps: Mismatches: Indels: -----Gln ------GCGTGCGCGCG ----cccage 493 433

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research to probes, for as enabling

identify other, similar proteins. They can also be used example in genetic screening, and in drug screening, as the production of animal disease models.

as well

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                                The present sequence
                                                  Example 3; column 633-672;
                                                                      Novel DNA fragment encoding human for identifying mutations and for disease states
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20-APR-1993;
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quence is a subunit (designated NMDARIA) of the human artate (NMDA) receptor. This is an ionotropic glutamate contains cation-specific ligand-gated ion channels. The coding sequence can be used in disease diagnosis and
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                    ProProSer***SerLysSerAsnThrSerThrLeuCysArgAlaSerValThrArgSer
                                                                  TrpSerGlyProSerLeuLeuSerSer----SerSerProAspThrArgProThrTrp
                                                                                                              {\tt SerSerThrThrGlnCysProSerArgThrArgGlyAlaProProAlaArgSerTrpPhe}
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                                               CCGCCCGCGCCACCACCGAAGAGA-
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CACGCACGCCTGAGCCGGCCAGCCAGCATGCCGGCCGCCGCCGCCTCG CACGCACGCCCTGAGCCCGGCCGCCCAGCATGCCGGCCGCCGCCCCC ValalaargargLeuCysalaGlyLeuArgSerProArgalaAlaProArgargArgGly CACGCACGGCCGCCTGAGCCCGGCGCCCAGCCCTTACAATCCGGCGTGAACGGGGCGGCGT	AMPHOLEMENT IGAACACCCTACCGAGCGCCGCCGCCATCCATTCCGTGTACGTCA	ATACCCCACCCCACCCCACCCCACCCCACCCCACCCCA	ArgArgAla***AlaThrProTrp	ArgProAlaCysSerArgPheCysArgGlnProAlaCCGCCC	ACCTCCCCCTCTCCCCCCTTCCCCCCCGCGGTGCTGGGGCACTATGCGCGCGC	NGCGGGCCGACGACGATGATCGGCTCCGACGGCC- ::::::	SerThrGlySerCysAlaThrArgCysPro	: : :	erSerThrCysCysTrp-	AGGACCGCGTGCTGCTGCGGACGCACCATCATCACCTGGTGCAAGCCCTTCCTCAACACCTGGTGCAAGCCCTTCCCCGAACACCTGGTGCAAGCCCTTCACCTGACCACCTGGTGCAAGCCCTTCCCCCAACACACCATCACCTGGTGCAAGCCCTTCCTGTGCAAGCCCTTCCTGTGCAAGCCCTTCCTGTGCAAGCCCTTCCTGTGCAAGCCCTTCCTGTGCAAGCCCTTCCTGTGCAAGCCCTTCCTGTACACCTGTGCAAGCCCTTCCTGTGCAAGCCCTTCCTGTGCAAGCCCTTCCTGTGCAAGCCCTTCCTGTGCAAGCCCTTCCTGTGCAAGCCCTTCCTGTGCAAGCCCTTCCTGTGCAAGCCCTTCCTGTGCAAGCCCTTCCTT	CGCTGGACGCGT- LBArgMetArgArgThrArg*	::: SerSerTrpGlyThrGluAr	AlaSerProCysArg AGGACGTCT	GCGAGACGCTGCCGCTGATCGAGGCCGCCA-	ThrargalaalaSerTrpSerProLeuGlyLeuAlaargSerLeuLeuProLeuAla	roGlySerTrpMetProSerSerMetMe	CCGCGAGCTGG	3	TGGCCGCGCTGGAGG	ArgserglyThrseralevelThrovalTh	PheSerGlyLeuLysIleSerThrHisLeuSerAlaSerAlaArgCys
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Novel nucleic acid encoding human N-methyl D-aspartate receptor 2A subunit, useful for expressing the subunit and as probes in genetic screening techniques, to identify patients having neuropathological conditions	WPI; 2002-096550/13. N-PSDB; ABA05910.	Daggett LP, Lu C;	(MERI) MERCK & CO INC.	20-APR-1994; 94US-0231193. 20-APR-1993; 93US-0052449.	29-SEP-1997; 97US-0940035.	13-NOV-2001.	US6316611-B1.	Homo saplens.	Human; N-methyl D-aspartate receptor; NMDAR; genetic screening; glutamate receptor; drug; modulator; receptor.	Human NMDA receptor subunit SEQ ID NO 44.	05-MAR-2002 (first entry)	ABB56523;	KESUIT 10 ABB56523 ID ABB56523 standard; Protein; 1081 AA. XX	865 AlaArgAlaArgValThrLeuProCysProAla	1694 GCATCG	845	1643 CCGAGCGCAAGGCCCGGAAAATGACCCTTCTAACAGGGGGGAAAATGACCCTTCTAACAGGGGGAAAATGACCCTTCTAACAGGGGGAAAATGACCCTTCTAACAGGGGGAAAATGACCCTTCTAACAGGGGGAAAATGACCCTTCTAACAGGGGGAAAATGACCCTTCTAACAGGGGGAAAATGACCCTTCTAACAGGGGGAAAATGACCCTTCTAACAGGGGGAAAATGACCCTTCTAACAGGGGAAAATGACCCTTCTAACAGGGGGAAAATGACCCTTCTAACAGGGGGAAAATGACCCTTCTAACAGGGGGAAAATGACCCTTCTAACAGGGGGAAAATGACCCTTCTAACAGGGGGAAAATGACCTTCTTCTAACAGGGGGAAAATGACCCTTCTAACAGGGGGAAAATGACCCTTCTTCTAACAGGGGGAAAATGAACCCTTCTTCTAACAGGGGAAAATGAACCCTTCTTCTAACAGGGAAAATGAACCCTTCTTCTAACAGGACGAGGAAAATGAACAGGAAAATGAACCCTTCTTCTAACAGGAAAATGAACAGGAAAAATGAACAGGAAAAATGAACAGGAAAAATGAACAGGAAAAATGAACAGGAAAAATGAACAGGAAAAAATGAACAGGAAAAAATGAACAGGAAAAAATGAACAGGAAAAAAAA	831 SerArgSerSerArgS	1601	811 ArgProArgAlaValThrThrAlaProPheLeuGluproThrAssProAlsals	1592 CGGCCCAC	791 GlyGlyArgCysGlyProGlyThrAlaGlyGlyThrSerArgProProSerGlyProCyc	1532 GCCGCCCCCCCAACCCTGGACGCAAACCGCTACATGGCCCCTTCCCTTCCCCTTCCCCTTCCCCAACCCTGGACGCAAACCGCTACATGGCCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCTC	774 ArgProCysProThrSerProGluCysArgAlaAlaGlnPro

Example 3; Column 265-272; 206pp; English.

The invention relates to nucleic acids (I, AA199167-AA199196, ABA05910) encoding human N-methyl D-aspartate receptor (NMDAR) subunits. The nucleic acids are useful for the production of NMDA receptor subunit isolate nucleic acids encoding related receptor subunits. Genetic screening can be carried out using the nucleotide sequences as probes to endogenous glutamate receptors. Also, patients having a family history of the determine if any abnormalities exist with respect to any of the disease states related to glutamate receptor dysfunction can be screened Expression vectors comprising (I), receptor subunits encoded by (I) and subunits and in specific combinations, as well as antibodies to the

Qy (P 29	쁑	Qy Qy	6 B 7	S B 7	ov D	o p	0 p	Qy .	를 ⁵	₽ .	Q B	Qy	β δ	р Б 5	- 1	Alig Pred Scor Perc Best Quer DB:	22222222X3
20 CCGCCCGCGCCACCACC	CCAGCGGCCCATCGGCATTTCGACCGGCGCCTTCTACCCGC	90 SerSerThrThrGlnCysProSerArgThrArgGlyAlaPro	70 ArgSerProGlyAlaGlnLeuSerLeuSerAlaSerProCysGlyCysCysGlyArgTrp 3	ProSerSerCysSerSerThrSerAlaLeuSerAlath	35 CysGly	26 ProserTrpSerHisIleAlaLeu	ACC. TGC TGG ACC AGC CAGC CAGC CAGC CAGC CAG	31	TIPTIOSETALBPTOSETPTOSETMETATGASNALBPTOATGSET***ThrSe TGCTCAGGCGTCGCGACATGACGCCCAAGATCTCGCAGGGCGTCACCACGGTGGTCACG	GGCCTGGTGGTCGCCCCGGCTTCATCGACTCCCACACCCACGACGACAACTACC 25	70 TY	S	13 GGCGCGCGACCTGG12	GGCGGCACCCTCATCGACGGCAGCAACACCCCGGGGC 11	32 CCATGTCCCCCCAGC 55	10-009-782-1 (1-1758) x ABB56523 (1-1081)	gnment Scores: 2.11e-18	receptor subunits substantially free of contamination from many other receptor proteins whose presence can interfere with analysis of a single NMDAR subtype. The availability of desired receptor subtypes allows the observation of the effect of a drug substance on a particular receptor subtype or combination of NMDAR subunits and to perform initial in vitro humans, a human NMDAR subtype or the combination of NMDAR subtype or the system that is specific for Sequence 1081 AA;

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TACCGAGCGCGCCGGCATCCATTCCGTGTACGTCA 1411	GGTGTTCGACCCGGCCACGGTGGCCG 1351 		GAAGATGACCGGCCTGACCG 1264	GCGGGTGCTGGGGCACTATGCGCGCG 1210 	CTCCGACGGCCTGCCGCACGACG 1150		GCGCGGCAAATCCAAGTACGACGTGG 1036 :::::: !ysTrpSerSerProGlySerThrTrp 626	CACCTGGTGCAAGCCCTTCCCCGAAC 976	ATCCCTACGTGGCCGGCTCCACCATGCTCAAGC 916 ::: ::: AlaAlaSerTrpThrSerThrThrTrpGluAla 605	luArgHisArgAsnTrpArgGlnCysGlySerGlnGlySer 585	TGGCGCGCC ::: erGlyPro***ThrTrpArgSer	GGGCCAGCCCAATTTCGGCCGCTCGC	ACGTGCCGGTGGTGATCTCGC 784 ::: ::! uLeuSerSerThrThrTrpGlnAlaArg 527	ו עב	CGCGCATGGCGGCATCTACGCCACCCACATGCGCGACGACGAGGCGAGCAGATCG 721	TCATCGAGGTGTGCCGGC 661 ::: erAlaSerAlaArgCysbroThrAlaAla 467	rLeuCysArgAlaSerValThrArgSer 447	

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       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, and polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
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                                                                                                                                                                               Claim 20; SEQ ID No 33892; 103pp; English.
                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations tesponsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                        N-PSDB;
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23-AUG-2000; 2000US-0649167.
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DB; AAS67720.
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The present invention relates to toluene degrading enzyme genes and proteins tutH (see AAP23629 and AAB59831), tutI (AAF23630 and AAB59832), tutI (AAF23631 and AAB59832), tutI (AAF23631 and AAB59833) and tutI (AAF23632 and AAB59834). The toluene degrading enzymes are homologues of pyruvate formate lyase. The toluene degrading enzymes are useful for biological treatment of organic compounds and in particular for the degradation of toluene and its enalogs contained in liquid or solid waste source. The present sequence is a protein sequence encoded by toluene degrading enzyme gene, TutD/E.	Disclosure; Fig 12; 122pp; English.	Composition comprising toluene degrading enzyme useful for biological treatment of organic compounds, especially for degrading toluene or its analogs	WPI; 2001-041080/05. N-PSDB; AAF23627.	Coschigano PW;	(UYOH-) UNIV OHIO.	01-JUN-1999; 99US-0323872.	24-MAY-2000; 2000WO-US14298.	07-DEC-2000.	WO200072650-A2.	Thauera aromatica. Xanthomonas maltophilia. Geobacter metallireducens. Azoarcus tolulyticus.	Toluene degradation; enzyme; waste degradation; TutE; TutD.	Protein #4 encoded by TutD/E gene.	04-APR-2001 (first entry)	AAB59827;	RESULT 12 AAB59827 ID AAB59827 standard; Protein; 1592 AA.	606 Thr 606	37 ACA 35	82 TGCCGCCCGCGAGCAGCAGGTCGAAGGGCTGGGAATCGGATTGGG 38		103 TGTTGCTGCCGTCGATGAGGG 83	546 TrpProLeuProSerArgProProGlySerGlyLysArgGlyAlaSerAlaProProGly 565	GlyArgArgAlaArgLeuProArgThrArgGlyProProArgProAlaProSer		513 AlaArgGly		504ArgGlyArgArgAlaGlySerAlaArg 512

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         The present invention relates to toluene degrading enzyme genes and proteins tuth (see AAF23629 and AAB59831), tuti (AAF23630 and AAB59832), tuti (AAF23631 and AAB59832), and tutie (AAF23632 and AAB59834). The toluene degrading enzymes are homologues of pyruvate formate lyase. The compounds and in particular for the degradation of toluene and its analogs contained in liquid or solid waste source. The present sequence analogs to the contained in liquid or solid waste source. The present sequence
                                                                                                                                                                                                         Disclosure; Fig 5; 122pp; English.
                                                                                                                                                                                                                                                                 Composition comprising toluene degrading enzyme useful for biological treatment of organic compounds, especially for degrading toluene or its
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Azoarcus tolulyticus.
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for toluene degrading enzyme,
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251 aHisArgArgCysThrAlaArgArgGlyArgPheArgGlyProThrSerArgAspThrGl
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US-10-009-782-1 (1-1758) x AAB59826

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Indels: Gaps:

Best Local S Query Match: Percent Similarity:

Similarity:

1.42e-15 331.50 36.65% 28.12% 10.05%

Length:
Matches:
Conservative:
Mismatches:

1615 178 54 203 198 36

Alignment Scores:

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                The present invention relates to toluene degrading enzyme genes and proteins tutH (see AAF23629 and AAB59831), tutI (AAF23630 and AAB59832), tutF (AAF23631 and AAB59832) and tutF (AAF23631 and AAB59834). The toluene degrading enzymes are homologues of pyruvate formate lyase. The toluene degrading enzymes are useful for biological treatment of organic compounds and in particular for the degradation of toluene and its analogs contained in liquid or solid waste source. The present sequence analogs contained in sequence degrading enzyme gene, TutD/E.
 Sequence
                                                                                                                                                                                  Disclosure; Fig 12; 122pp; English.
                                                                                                                                                                                                                         Composition comprising toluene degrading enzyme useful for biological treatment of organic compounds, especially for degrading toluene or i
                                                                                                                                                                                                                                                                                              N-PSDB;
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Geobacter metallireducens
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Homo sapiens. WO200175067-A2.	Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.	Novel human diagnostic protein #3521.	T 13-FEB-2002 (first entry)	X	രശ	b 1018 AlaArgArgProValIleSerArgArgSerPro 1028	1679 TGTCGCAG	1001LysSerArgSerMetThrAlaThrThrGlyArgThrProThrCysAsnSer	1622 TGATGGGCGCGCGCGCGCGCGCGAGCGCGAAAGGCCCCGGAAAATGACCCTGCAAGACACC	984 ysLys-ProvalArgLysValAlaAlaGlnSerSerArgProserCysTrp	1565 ACATGGCCCCTCCCCTCGCAATACGGCCCCACCCGATATCGTGGGCAAGGAAG	965ThrThrGlySerThrCySCySAlaCySArgProAlaSerThrValAlaAlaArgArgL	1505 TACAATCCGGCGTGAACGGGGGGGGGGGGCGCCCCCTCCCAACCCTGGACGCAAACCCTG	Db 946 ArgArgAsnThrProSerSerAlaSerThrAlaThrAlaProProThrArgLysPro- 964	1445 CCGGCCAGCATGCCGGCCGCGTGCTCGCACGCACGCACGC	926 SeralaseralaThraspSeralaIleArgArgSerSerThrThrarceraliance	1409TOARCGGCGCGCGCGCTCGGTCTGGC	906 ProProSerSerSerAlaIleProArgArgThrAlaA	1385 CCGCCGGCATCCATTCCG		1346 TGGCCGATACCGCCACCTTCGAACACCCTACCGAGC	870 ThrileCysSerSerSerSerAlaAlaProThrProArcalsarc	1304	852	1250 TGACCGGCCTGACCGCCGCGCGCTTCGGCCTGGCCGGGCCGGGCCGGCGCGCGCGCGCGCGCGCGCGCGCG	838 ThripMetargTipAsnSerSerArgTrDAsnValArgPha	1190 TGCTGGGGCACTATGCGCGCGACCTGGGGCCTGTTCCCGCTGGAGACGGCCGTTATGGAAGA	818	1130 CCGACGGCCTGCCGCACGAGCGCCCGCATCCGCGCCTGTGGGGCACCTTCCCGCGCGC	801	1070 TCATGATGGACGAACCCGACGTGCAGCGCATCCTGGCGTTCGGCCCCGACCATGATCGTCCT	785 SerProAlaArgAlaSerArgThrArgCysArgAsgAsgAsgErLeuPro	QY 1010 AGCGCGGCAAATCCAAGTACGAGGTGGCCGGAGCTGCAGCCGGCCG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polyperase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC are to restore normal activity of (II) is useful in gene therapy techniques CC (II), (II) is useful for generating antibodies against it, detecting or CC a food supplement. (II) and its binding partners are useful in medical CC disorders involving abarrant protein expression or biological activity. CC disorders involving abarrant protein expression or biological activity. CC dispositics, forensics, gene mapping, identification of mutations in CC responsible for genetic disorders or other traits to assess biodiversity amino acid sequences. ABG00010-ABG30377 represent novel human CC Note: The sequence data for this patent did not appear in the printed after the sequence data for this patent did not appear in the printed after the sequence data for this patent did not appear in the printed after the sequence data for this patent did not appear in the printed after the sequence data for this patent did not appear in the printed after the sequence data for this patent did not appear in the printed after the sequence data for this patent did not appear in the printed after the sequence of the invention.
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Best Local Similarity:
Query Match:
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                                              79 ProAlaSerAla-----AlaTrpGlyAlaGluGlnGluProValArgSerTrpGlyPro 96
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                                                                                                                                                                                                                                                                    41 AlaAlaGly***ArgArgMetTrp-----CysAlaSerAlaSerLeuAla***SerPro 58
                                                                                                                                                                                                                                                                                                                                                                                   21 SerProAlaProGlyCysArgArgAlaAlaProArgTrpSerSerProGlyProArgThr 40
                                                                                                                                                                                                                                                                                                                                                                                                                53 AGCCCTTCGACCTGCTGGTCGCGGGGGGGGCACCCTCATCGACGGCAGCAACACCCCGG--- 109
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N-PSDB; AAS67717.
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23-AUG-2000; 2000US-0649167.
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Search completed: May 11, 2003, 12:09:19 Job time: 97 secs

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ALIGNMENTS

FEATURES Source	,	JOURNAL COMMENT	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BG809984 LOCUS DEFINITION
Email: ralph_dean@ncsu.edu Seq primer: T3 primer (AATTAACCCTCACTAAAGGG). Seq location/Qualifiers 11516 /organism="Magnaporthe grisea" /strain="70-15"	Fungal Genomics Laboratory North Carollina State University Campus Box 7251, Raleigh, NC 27895, USA Tel: 919-513-0020 Fax: 919-513-0020	Consequence analysis of an appressorium stage cDNA library in the rice blast fungus, Magnaporthe grisea Unpublished (2001) Contact: Ralph A. Dean	Eukaryota; Fung1; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. 1 (bases 1 to 1516) Choi, W. and Dean, R.A.	EG809984.1 GI:14180964 EST. Magnaporthe grisea. Magnaporthe grisea	BG809984 1516 bp mRNA linear EST 22-MAY-2001 mgct002xd1lf Magnaporthe grisea Appressorium Stage cDNA Magnaporthe grisea CDNA clone mgc+002xd11f f / mayn

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="vector: pBlueScript SK(+) vector; Site_1: EcoRI; Site_2: XhoI; The appressorium formation-specific cDNA library was constructed from conidia germinated for 5-8 hr on an inductive surface. The library contains over 55,000 clones with average insert size of 1.5 kbp."

a 657 c 660 g 16 t 118 others
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/clone=lb="Magnaporthe grisea Appressorium Stage cDNA"
/dev_stage="Germinated conidia on appressorium-inductive
surface"
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     Pan troglodytes DNA, clone:
1798 bp DNA linear one: RP43-040F09.TJ, genomic
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JOURNAL REFERENCE REFERENCE AUTHORS VERSION KEYWORDS ACCESSION TITLE JOURNAL AUTHORS ORGANISM Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22, Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-chou Tsurmin', Schwinz Schenes Center (GSC); (E-mail:chimpbes@so.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/.Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors. Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y. BAC end sequences of Library RPCI-43 Eukaryota; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae. Pan troglodytes Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee Male BAC Library clone:RP43-040F09.TJ AG171124.1 sequence. 1 to 1798) GI:16700802 Taylor, T.D.,

Hominidae;

Euteleostomi;

Yada, T.,

SOURCE

LIBRARY R.Site 1 R.Site 2 Vector /organism="Pan troglodytes" /db_xref="taxon:9598" Location/Qualifiers : pBACe3.6 : ECORI : ECORI.

COMMENT

PRIMERS

Sequencing: TJ

TITLE

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Best Local Similarity

Matches 645; Conserv
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                           CCTACGTGGCCGGCTCCACCATGCTCAAGCAGGACCGCGTGCTGCTGGCCGGACGCACCA
                                                                  AAGGCGAGCACATCGTGGCCGCGCTGGAGGAAACCTTCCGCCATCGGCCGCGAGCTGGACG
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ilarity 38.6%;
Conservative
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/sex="male"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
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Pred. No. 0.00037;
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                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-040F09.TJ.
Pan troglodytes
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JOURNAL REFERENCE AUTHORS

Unpublished

2 (bases 1 to 1798) Fujlyama, A., Hattori, M., Totoki, Y., Watanabe, H. a

and Sakaki,Y.

Yada, T.

Submission

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CGAAGGCGAGCACATCGTGGCCGCGCTGGAGGAAACCTTCCGCATCGGCCGCGAGCTGGA
                                                 CGCGGGGCGGCGNNGNGCGCCGNGCGGGCGNGGCGGGGGCGCGCGCGGNNC-GCGCGG
                                                                        CATCGGCATTTCGACCGGCGCCTTCTACCCGCCGCCGCCGCGCGCCACCACCGAAGAGAT
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                                                                                                                                                                                                                                                                                                                                                        TCTCGCAGGGCGTCACCACGGTGGTCACGGGCAATTGCGGCATCAGCCTGGCCCCGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-AUG-2001) Asso Fujlyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
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/clone="RP43-040F09.TJ"
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                      Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-007N10.F.
Pan troglodytes
                                                                             AG032943

Pan troglodytes DNA, clone: PTB-007N10.F, AG032943
                                                                  AG032943.1
   Mammalia; Eutheria;
              Eukaryota; Metazoa;
                                                                  GI:16559816
  Chordata;
Primates;
 Craniata; Vertebrata; Catarrhini; Hominidae
Hominidae;
                                                                                  genomic survey
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VERSION KEYWORDS SOURCE ACCESSION DEFINITION Snoor

REFERENCE

AUTHORS

Fujiyama,A.,

BAC end sequences of Library

lyama, A., Hattori, M., Toyoda, A., Coki, Y., Watanabe, H. and Sakaki, Y.

Taylor, T.D.,

Yada, T.,

TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 330-0045, Japan Direct Submission Fujiyama, A., Hattori, M., Totoki, Y., Watanabe, H. (bases 1 to 1542) ., Toyoda, A., and Sakaki, Y. Taylor, T . . Yada,

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les 329; Conserv
TGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCATCGGCATTTCGACCGGCGCCCT
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                                             Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY
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/clone_lib="PTB Chimpanzee Male
657 c 614 g 19 t :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism-"Pan troglodytes"
/db_xref-"taxon:9598"
/clone-"PTB-007N10.F"
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CCGCGCTGGAGGAAACCTTCCGCATCGGCCGCGAGCTGGACGTGCCGGTGGTGATCTCGC
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                                                  TGAGCGCGCATGGCGGCATCTACGCCACCACATGCGCGAAGGGCGAAGGCGCACATCGTGG
                                                                                            GGCGCGCGCGCGCGCGCGCCCCCGCGCGNGGGGGGGNGCGCCCGCGNCGCGCGCGCGC
                                                                                                                         ACAAGGTCATGGGCCAGCCC
                              463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB Innuhitehad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-911, Fax:81-45-503-9170)
Tel:81-45-503-911, Fax:81-45-503-9170
Clones are derived from the chimpanzee BAC library PTB This BAC encass generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan troglodytes DNA, clone: AG030608
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                                                                                                                                                                                                                                                                                Similarity 41.4
63; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing: M13Rev
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R.Site 2
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/cell_type="lymphoblast"
/clone_lib="FFB Chimpanzee Male
/clone_lib="540 g 24 t 1
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/db_xref="taxon:9598"
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Pred. No. 0.0045;
0; Mismatches 625
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Fax: 919-513-0024
Email: ralph_dean@ncsu.edu
Emqil: T3 primer (AATTAACCCTCACTAAAGGG).
Seq primer: T3 primer (AATTAACCCTCACTAAAGGG).
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North Carolina State University
Campus Box 7251, Raleigh, NC 27695,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 construction and sequence analysis of an appressorium stage library in the rice blast fungus, Magnaporthe grisea Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Ralph A.
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a 380 c 561 g 10 t 106 others
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; on bw sp, the same strain used for the BDGP's and box to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be coation/Oualifiers

Location/Oualifiers
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 925)
                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIOSOPHIE 925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                      /clone="BACR19D16"
/clone_lib="RPCI-98"
/note="end : TET3"
61 c 61 g
                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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                                                                                               4.18;
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                                                                                           Score 72.4; DB 17;
Pred. No. 0.017;
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                                                                        Mismatches
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                                                                                                                                                                                                                                                                    Submitted (02-AUG-2001) Asso Fujlyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbose@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC endwas generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 1299)
Fujiyama, A., Hattori, M., Toyoda, A.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y. BAC end sequences of Library PTB
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AG039481.1 GI:16568206
GSS.
Pan troglodytes male lyn
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R.Site 2
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 /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
571 c 592 g 31 t 81 others
                                                            /sex="male"
                                                                                        organism="Pan troglodytes"/db_xref="taxon:9598"
                                                                          clone="PTB-016J15.F"
                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria;
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Eutheria; Primates; Catarrhini; Hominidae;
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Query Match

4.18;

Score 72.4;

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RESULT 9
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   Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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Drosophila melanogaster genome sur
BACR14B09 of RPCI-98 library from
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                                                                             genomic survey sequence.
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Survey sequence T7 end of BAC #
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AG030611
Pan troglodytes DNA,
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1341 bp DNA clone: PTB-003A20.F,

linear genomic

GSS 01-NOV-2001 survey sequence.

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564 CSCCSCSMSCCCCCGCASCVCAGCCMSAGCMGCGCCMCCCGCCASCGSCCSCCCYCGBCC
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                                  GGGCGGCGTGCCGCCCTCCCAACCCTGGACGCAAACCGCTACA 1567
CCCCGGCMGCMYGCCMCCCMGVMACCMGCGVGMMGMCMGMGRCV
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                                                                                             CCGSCGCCCCYGSCCSGGSCSSCCGCCMCMVARMAVSVSCCCCCCSCCMASCCCCGCVSG
                                                                                                                                                                                                                           CGSSGCCGGCSCSCCSSGCCSSGCSSGCGCGCGCGSCGSGSGCGSSSSCCCGCGCCS
                                                                                                                                                                                                                                                              collaboration with the Berkeley Drosophila Genome project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Cancer Genetics at the Roswell Park Cancer Tstitute in Buffalo, ECORI digestion of Drosophila DNA provided by partial isogenic strain y2; cn bw sp. the same strain used for the BDGP's and how to order individual BAC clones, the entire library filters for hybridization from the BACPAC Resource Center can be Location/Onal ifface.
                                                                                                                                                                                                                                                                                                                             GGGCGCGGGCAGCTGCAG--GCCGGGTACTTCGGCCGACCTGGTGGTGTTCGACCCGGCCA 1342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail : - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was collaboration with the Berkeley Drosophila
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Best Local Similarity

Matches 245; Conserv
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                             CGCGTGCTCGCACGCCACGGCCGCGTGAGCCCGGCGCGAGCCCTTACAATCCGGCGTGAAC 1521
GTGGCCGATACCGCCACCTTCGAACACCCTACCGAGCGCGCCGCCGGCATCCATTCCGTG 1404
                                                                                                                                                                                      GGGCGCGGCCAGCTGCAGGCCGGGTACTTCGCCGACCTGGTGGTGTTCGACCCGGCCACG 1344
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                                                                                                                                                                                                                                                                                                               CGCCTGTGGGGCACCTTCCCGCGGGTGCTGGGGCACTATGCGCGCGACCTGGGGCCTGTTC
                                                                                                                          (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fullyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y.
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/cione_lib="77B Chimpanzee Male BAC Library"
476 c 700 g 14 t 103 others
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/db_xref="taxon:9598"
/clone="PTB-003A20;F"
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Eutheria; Primates; Catarrhini;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila nelanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Econi digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
                                       SSGTSSACVKCNASSSCGCCGCGNABCCMCSSSSSCCGSASARGVKVRASGGAGKRGGGS
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo

Reoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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Pred. No. 0.023;
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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
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Submitted (02-AUG-2001) Asao Fujlyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbesgac.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end

JOURNAL TITLE

Fujiyama, A., Hattori, M., To Totoki, Y., Watanabe, H. and

Toyoda, A., 'nd Sakaki, Y.

Taylor, T.D.,

Yada, T.,

Direct Submission

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                                                                    GCTTCGGCCTGGCCGGGCGGGGCAGCTGCAGGCCGGGTACTTCGCCGACCTGGTGGTGT 1330
                                                                                                                                                               AGCGCCCGCATCCGCGCCTGTGGGGCACCTTCCCGCGGGTGCTGGGGGCACTATGCGCGCG 1210
                                              GCCGCCGCGCGCCNGCCCCGCCCCNCNNCGCGCGCGCNNCNCNCCGCGGCCNGCCCGNNCG
                                                                                            ACCNCGGGCGCCGCGCGCGCGCGCCCGNNCGNNCGCGCNCGGCNCCGGCGCCCNCCGCGG
                                                                                                                 ACCTGGGCCTGTTCCCGCTGGAGACGGCGGTATGGAAGATGACCGGCCTGACCGCCGCGC 1270
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R.Site
R.Site
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/clone_lib="778 Chimpanzee Male BAC Library"
669 c 552 g 64 t 186 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-003A18.F"
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Pred. No. 0.03;
0; Mismatches 634;
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AG127788/c
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                                                                                                                                                                                                                                                                                                                                                      Submitted (02-AUG-2001) Asao Fujlyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC end
      Similarity 38.:
52; Conservative
                                                                                                                                                                                                                                                                                                                              clone tracking errors.
                                                                                                                                                                                                                                                                                                                                             was generated during the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pan troglodytes DNA, clone: AG127788 AG127788.1 GI:16656953
                                                                                                                                                                                                                                                                              Sequencing: M13Rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujlyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totokl, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
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Ammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                 R.Site 1
R.Site 2
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                                                                                                                                                                                                                                                                   /ector
                                                                        /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
/369 c 480 g 44 t 182 others
                                                                                                                                  /clone="PTB-138M02.R"
/sex="male"
                                                                                                                                                                                                                te 2 : SacI.
Location/Qualifiers
                                                                                                                                                                  /organism="Pan troglodytes"
/db_xref="taxon:9598"
                      4.0%;
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 Score 71; DB 1
Pred. No. 0.03;
0; M1smatches
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                  DB 17; Length 1129;
     565;
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                                                                                                                                                                                                                                                                                                                                      ee BAC library PTB This BAC end and may have higher chance of
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                                                                                                          NNNNNNNNNCCNNCCCANCGTGCGGCCTNNNNGGGGCCCGCACNNCNCCCCCCA 160
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Chlamydomonas reinhardtii.
                BG852363.1 GI:14233547
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756 CGAGCTGGACGTGCCGGTGGTGATCTCGCACCACAAGGTCATGGGCCCAGCCCAATTTCGG
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                                 CGAAGAGATCATCGAGGTGTGCCGGCCGCTGAGGGGCGTGATGGCGGCATCTACGCCACCCA 695
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Durham, NC 27708-1
Tel: 919 613 8159
Fax: 919 613 8177
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Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 1281)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
KhoI; This library, constructed by John Davies and Jeffrey
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/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
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Search completed: May 11, 2003, 10:48:47 Job time : 28329 secs

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; ORGANISM: Burkholderia mallei
US-10-282-122A-14027
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                                                                  TGCTATCCGTACAGCCGCAGCTCGTCGACGCTCGACATCAAGCAGGCGACGCGGCGACATC
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Pred. No. 2.1e-66;
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PRIOR APPLICATION NUMBER: 60/269,308
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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OR APPLICATION NUMBER: 60/206,848
OR FILING DATE: 2000-05-23
OR APPLICATION NUMBER: 60/207,727
OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: 60/230,335
OR FILING DATE: 2000-09-06
OR APPLICATION NUMBER: 60/230,347
OR FILING DATE: 2000-09-09
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                                                    APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/2253,625
FILING DATE: 2000-11-27
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 24070
LENCTH: 1437
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
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                      CCAGCTCATCGACGCTGGATATGAAACAGGTGACCGACGAGTTTGATATCGTGATCACCT
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                                               CCGGCTCCACCATGCTCAAGCAGGACCGCGCGCGCTGCTGGCCGGACGCACCATCATCACCT
                                                                          CCTTTTTCGATGAGATGCGCCAGCAGCAGGATATCGCCTGCGACTGTTATCCCTATTCAG
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Pred. No. 1.8e-57;
0; Mismatches 581;
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LENGTH: 1590

TYPE: DNA
ORGANISM: Streptomyces a:
FEATURE:
NAME/KBY: CDS
LOCATION: (1). (1590)
US-10-156-761-3269
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-262
CURRENT FAPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2007-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 3269
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CCGACGTCGGTATCACCGGCGGGCCGGATCGCCGAGATCCGCCGCGACGGCCCCGGCCCTGG
                             CCGACCTGGGCGTGCGGGGACCGCATCGCCGCCATCG---GCGATCTGTCGGACGCCG 175
                                                            TGGATCTCGTCATCCGTGATGTGCGCGTCGTCGACGGCACCGGCGGCGCGCGTCCTGCCGTG
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Similarity 50.3%;
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HORIKAWA, HIROSHI
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                                                                                                                           Score 161.2; DB 8;
Pred. No. 2e-16;
0; Mismatches 538;
                                                                                                                           Indels
                                                                                                                                                        Length 1590;
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CCGCCCGCCGGCTGCTCCTCGACGAC
                                               CCTACGTCGGCAGCACCGTCCAGGCCTCGGCCGACCTGCGCGGCGAGGCCCCCTGGACCA 1123
                                                                           CGACCATGATCGGCTCCGACGCCTGCCGCACGACGACGACCCCCCATCCGCGCCTGTGGG
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US-10-156-761-3783
J Sequence 3783, Application US/10156761
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 3783
LENGTH: 1728
TYPE: DNA
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FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1728)
US-10-156-761-3783
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Best Local Similarity
Matches 345; Conserv
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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                                                                                                                    CGGTCATGCCGGACTTGCAGCGCCGG------CCACCGACGAGGAAATCGCGGCCATGC 550
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                                                                             ACGTTATGGGCCCGGACGCGGTCGGCGGCCGGCCCACGCGGGAGCAGCTGGAGCGGATGC
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SAKAKI, YOSHIYUKI
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HORIKAWA, HIROSHI
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Pred. No. 9e-10;
0; Mismatches 221;
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PCT-US02-37547-12
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PCT-US02-37547-12
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GENERAL INFORMATION:

APPLICANT: Floss, Heinz
APPLICANT: Yu, Tin Wein
APPLICANT: Leistner, Eckard
TITLE OF INVENTION: Blosynthetic Gene Cluster for the Maytansinoid Antitumor Agent
FILE OF INVENTION: Ansamitocin
FILE REFERENCE: UMASH-06712
CURRENT APPLICATION NUMBER: PCT/US02/37547
CURRENT FILIG DATE: 2002-11-21
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.0

SEQ ID NO 12
LENGTH: 3354
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Best Local Similarity 44.2%;
Matches 758; Conservative
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                                                              CGCTCACCGCCTCCCGCCGCCCCACAACCCTCCACGCCTCCGCCCCCGCACACCCTCCGCCC
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Pred. No. 2.1e-09;
0; Mismatches 935
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                             AGCTGGGCCAGATCGCCCTGAGCTACGAGAAGCT 1757
CCCTGGCCGTCACCGGCCTCACCAACCGGCAGAT 3224
                                                          CGGCCGACCCCGTCGAGCACGACACCAGCGGCCTCACCGGCTCCGAGCGCAAGGTCGCCG
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GENERAL INFORMATION:
APPLICANT: Floss, Heinz
APPLICANT: Yu, Tin-Wein
APPLICANT: Yu, Tin-Wein
APPLICANT: Leistner, Eckard
TITLE OF INVENTION: Blosynthetic Gene Cluster
TITLE OF INVENTION: Ansamitocin
FILE REFERENCE: UWASH-06712
CURRENT APPLICATION NUMBER: PCT/US02/37547
CURRENT FILLING DATE: 2002-11-21
NUMBER OF SEQ ID NOS: 57
SOFTMARE: Patentin version 3.0
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Best Local Similarity 44.2%;
Matches 75%; Conservative
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                                                                                      CGCGCACCTCGGCCCACCCCACCCCCCCCCCCCCCCCCGAGCCGGCGTCGACCCGTGGT
TGGTGATCTCGCACCACGAGGTCATGGGCCAGCCCAATTTCGGCCGCCTCGCGCGAGACGC
                                                         ACATCGTGGCCGC----GCTGGAGGAAACCTTCCGCATCGGCCGCGAGCTGGACGTGCCGG
                                                                                                                  CGACCGGCGCCTTCTACCCGCCGCCGCCCCGCGCCACCGAAGAGATCATCGAGGTGT
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Pred. No. 2.1e-09;
0; Mismatches 935;
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CCCTGGCCGTCACCGGCCTCACCAACCGGCAGAT 72165
                         AGCTGGGCCAGATCGCCCTGAGCTACGAGAAGCT 1757
                                                CGGCCGACCCCGTCGAGCACGACACCAGCGGCCTCACCGGCTCCGAGCGCAAGGTCGCCG
                                                                           TGACCCTGCAAGACCTGTCGCAGGCCAGCGGCATCGCGGTCTCGACCCTGTCCAAGGCCG
                                                                                                     CGCTGCGCGCTCGCCGCTCAGCCCGCCGACCGCCGCACCTGCTCGCCGAGG
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RESULT 7
PCT-US02-37547-4:
; Sequence 4, Application PC/TUS0237547
; GENERAL INFORMATION:
; APPLICANT: Floss, Heinz

APPLICANT:

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CURRENT FILING DATE: 2002-11-21

NUMBER OF SEQ ID NOS: 57

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 9975

TYPE: DNA

ORGANISM: Actinosynnema pretiosum

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Best Local Similarity
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1194 GGGCACTATGCGCGCGACCTGGGCCTGTTCCCGCTGGAGACGGCGGTATGGAAGATGAC 1253
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APPLICANT: Leistner, Eckard
TITLE OF INVENTION: Biosynthetic Gene Cluster
TITLE OF INVENTION: Ansamitocin
FILE REFERENCE: UWASH-06712
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                                               CGGCTGGCCCGCGAGCGCCACGCGGCCGGCCTGCCCACCTCGATCGCCTGGGGCCT
                                                                           CGGCCTGCCGCACGACGACGCCCCCCATCCGCGCCCTGTGGGGCCACCTTCCCGCGGGTGCT 1193
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Pred. No. 3.4e-06;
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 6189
LENGTH: 2538
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ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2538)
US-10-156-761-6189
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Best Local Similarity 43.5
Matches 568; Conservative.
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                                                                                            ACCCTCGCCGACTTCATCGACTCCCTCGCCGCCGCCACCGAACGCGACGTCCACGCCTGG 1347
                              GCCGACTCCTGGCTGCGCACGACCGGCGTCGACACCCTGACCCCGGACATCACCACGGCC
                                                 GACATGACGCCCAAGATCTCGCAGGGCGTCACCACGGTGGTCACGGGCAATTGCGGCATC 330
                                                                                                                          GTCGCGCCCGGCTTCATCGACTCGCACACCCACGACGACAACTACCTGCTCAGGCGTCGC
                                                                                                                                                                                        GCCATCGGCGATCTGTCGGACGCCGCGCGCACACCCGGGTCGACGTGTCGGGCCTGGTG
                                                                                                                                                           GAGAAGGACTTCCTCGCCGGCATCAACACCCACTTCACCCGCCACAAGTTCGGCAACGCC
                                                                                                                                                                                                                          GCGCACCCCCGCCGACCTGCTCGCC 4746
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Pred. No. 1.6e-05;
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for the Maytansinoid Antitumor .

Length 4770; Indels

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Gaps

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Sequence 3, Application PC/TUS0237547
GENERAL INFORMATION:
APPLICANT: Floss, Heinz
                                                                                                                                                                                                                                   2248 AACTACCTGTTCACCGCCACGCCCAGGGCTTCTGGCAACCGGAACAGGCCGACCTCGTA
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                                                                                                                                            GCCATCGCCGCCGCGGGGCCGCTGGGCCTTCCCCGCCCACGCCGT 2414
                                                                                                                                                                           GCCGGGCGCGGCAGCTGCAGGCCGGGTACTTCGCCGACCTGGTGGT 1328
                                                                                                                                                                                                       CGCGCCTACGTCGAGCGGTACTGGACCGACGCGGTCGCCGTCGCCGCCGCCGCGCCCCC
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Best Local Similarity
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3801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yu, Tin-Wein
APPLICANT: Leistner, Eckard
TITLE OF INVENTION: Blosynthetic Gene Cluster
TITLE OF INVENTION: Ansamitocin
FILE REFERENCE: UMASH-06712
CURRENT APPLICATION NUMBER: PCT/US02/37547
NUMBER OF SEQ ID NOS: 57
NUMBER OF SEQ ID NOS: 57
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ORGANISM: Actinosynnema pretiosum
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                                              GCACGGCCGCCTCGCCACCTCCGTCGCCTGGGGCGCCTGGGGACGGCGGCGGCATGTCCAG
                                                                                                                              GACGCTGCCGCTGATCGAGGCCGCCATGGCGCCCAGGACGTCTCGCTGGACGCGTATCC
                                                                                                            GCGCCCGCTCGACGCGTTCGTCCTGTTCTCCTCCAACGCGGGCGTGTGGGGGCAGCGGCGG
                                                                                                                                                                                                       AGGCGAGCACATCGTGGGCGCGCGGGAGGAAACCTTCCGCATCGGCCGCGAGCTGGACGT
                                                                                                                                                                                                                                    CGCGCGCGTCCAAGGCCGCCAAGGCGCTCGGCGAGCACCTCGACGAGCTGCTGGGCGG 3800
                                                                                                                                                                                                                                                                                                                                                                                  CGAGGAAATCGCGGCCATGCGG---GACCTGGCCGAGGAAGCCATGGCCAGCGGCGAGT 587
                                                                                                                                                                                                                                                                    CGAGGTGTGCCGGCCGGTGAGCGCGCATGGCGGCATCTACGCCACCACATGCGCGACGA 707
                                                                                                                                                                                                                                                                                                   CGTGCACGCGGCGGGGGGCCAACGCCCAGACCCCCGTCGCCGACACCACCCCCGAGGAGCA 3740
                                                                                                                                                                                                                                                                                                                          CGGCATTTCGACCGGCGCCTTCTACCCGCCGCCGCCGCCGCCGCCACCGAAGAGATCAT 647
                                                                                                                                                                                                                                                                                                                                                                CGCCGACCTGGAGGCGCTGGGCGCCGCGTCACCACCGCCGCCTGCGACGTCGCCGACCG
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Pred. No. 2.2e-05;
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APPLICANT: Yu, Tin-Wein
APPLICANT: Leistner, Eckard
TITLE OF INVENTION: Biosynthetic Gene Cluster
TITLE OF INVENTION: Ansamitocin
FILE REFERENCE: UWASH-06712
CURRENT APPLICATION UMBER: PCT/US02/37547
CURRENT FILING DATE: 2002-11-21
NUMBER OF SEQ ID NOS: 57
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                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 460; Conser
                                                                                                                                                                                                                                                                                                                                SOFTWARE:
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                    10998
                                                                                                                                                                                                                                                                            LENGTH: 14055
TYPE: DNA
ORGANISM: Actinosynnema pretiosum
-USO2-37547-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    equence 1, Application PC/TUS0237547
ENERAL INFORMATION:
                                                                                                           10938
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504 GCCGGACTTGCAGCGCCGCCACCGACGAGGAAATCGCGGGCCATGCGGGACCTGGCCGA
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                                        GCCGGCGGCCGTCAACGCCGCCTGTATGGTGGGCCATTCAACGCTGCGCGCCGCCGGTCAT
                                                                                              CGAAGGCGGCTCTTACCGTTTCGAGCGCTTCGCCGACTACCTGGACGCGTTGCGGGCCAC 443
                                                                                                                                                      CGACACCCGCTACGCGCAGGCCGGCCTGTTCGCCGTGCAGGTCGCGCTGCTGCTGCTGCT 10937
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                                                                                                                                                                                                             Score 88.4; DB 1;
Pred. No. 4.1e-05;
0; Mismatches 561;
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                                                                                                                                                                                                                                         Length 14055;
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RESULT 11 PCT-US02-37547-2

Sequence 2, Application GENERAL INFORMATION: APPLICANT: Floss, Heinz APPLICANT: Yu, Tin-Wein

PC/TUS0237547

APPLICANT: YU, TIN WELL
APPLICANT: YU, TIN WELL
APPLICANT: Leistner, Eckard
TITLE OF INVENTION: Blosynthetic Gene Cluste:
TITLE OF INVENTION: Anaamitocin
FILE REFERENCE: UWASH-06712
CURRENT APPLICATION NUMBER: PCT/US02/37547
CURRENT FILING DATE: 2002-11-21
NUMBER OF SEQ ID NOS: 57
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn version 3.0

Gene Cluster

for the Maytansinoid Antitumor

Agent

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              GGCCACGGTGGCCGAT 1353
                                                                       CCTGGCCGGGCGGCAGCTGCAGGCCGGGTACTTCGCCGACCTGGTGGTGTTCGACCC 1337
                                                                                                   GATCCCCGGCTCGGACACCGCCGCGCTTCACCGGCCGCCGCCGCCACCGGCGCGCCCACCCGTG
                                              GCTGGCCGACCACCGGCTGCTCGACGCGGTCGTCGTGCCCGGCACGGCCCTGCTGGACCT
                                                                                                                           CCTGTTCCCGCTGGAGACGGCGGTATGGAAGATGACCGGCCTGACCGCCGCGCGCTTCGG
GGTGCGGGCGGCCGGT 11904
                                                                                                                                                       CGCCCCCCCACCACCGACGCCCCCCCCCCGCTGGAGCACCCGCTGCTCACCGGGGAGCTGGA
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; LENGTH: 9222
; TYPE: DNA
; ORGANISM: Actinosynnema pretiosum
PCT-US02-37547-2
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Best Local Similarity 43.8%;
Matches 614; Conservative
7942 GCGCCTCGGGGCGGCGGCCGACCGTGCTGGAGGTGGGGCCGACCGCCTCGGCCGAG 8001
                                                    7882 TTCTGGCCCGCGCGCAGGCGCCCGGCGCGTGGTGCGAGGTCCGCCTGGAGCGGTTGCCC
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                                                                                                          CTGCTGGGCGGGCCGGGGCGGTCGTCGACCTGCCCACCTACCCGTTCCAGCGCACCAGG
                                                                                                                                  CTGGCGTTCGGCCCGACCATGATCG--GCTCCGACGGCCTGCCGCACGACGACGACGCCCCC
                                                                                                                                                             GGGCTGCTCTCCGGGATCGGCGACCTGTTCGCGTCCGGGGCCCCGGTCGACTGGACCGCG
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Pred. No. 0.0001;
0; Mismatches 772; Indels 15
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APPLICANT: STAFFA, Alfredo
TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEP
FILE REFERENCE: 3002-110S
CURRENT APPLICATION UNMBER: US/10/329,079
CURRENT FILING DATE: 2002-12-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
SEQ ID NO 12
LENGTH: 15738
TYPE: DNA
ORGANISM: Streptomyces fradiae
US-10-329-079-12
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; Sequence 12, Application US/10329079
; GENERAL INFORMATION:
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Best Local Similarity 43.1%; Pred. No. 0.00033;
Matches 580; Conservative 0; Mismatches 749;
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1354 CTGGAGGAGTTCGCCGCGAGCCCGCAGCCGAGCCCGCAGCCGCCGAGCCCGCGGCC 1413
                                                                                      1294
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                                CACACCCACGACGACAACTACCTGCTCAGGCGTCGCGACATGACGCCCAAGATCTCGCAG 294
                                                                  GCCCCACCGTCCCCCGGGGCTCGGGGAACGCCTCGTCCGCCTGCTGGAGGCCCGGCACCGCC
                                                                                                   GCGCGCACACCCGGGTCGACGTGTCGGGGCCTGGTGGTCGCCCCGGCTTCATCGACTCG 234
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                          GCCTACGTCCTCGACGCGGGACTGCGGCCGGTCCCGGCCCGGCGTGCTGGGCGAGCTGTAC
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CURRENT FILING DATE: 2002-12-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 37360
TYPE: DNA
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Best Local Similarity
Matches 580; Conserv
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GENERAL INFORMATION:
APPLICANT: FARMET, Chris
APPLICANT: ZAZOPOULOS, Emmanuel
APPLICANT: STAFFA, Alfredo
TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTI
FILE REFERENCE: 3002-11US
                                                                   15990
                                                                                                                                                                                                   15870 GTCCACGTACCGCTGGACCCACGCTCCCCGCACGAGCGGCTGGCCGCCGTCGAACGCGAC
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                                                       GCCCCGGTCCTCGTCCTGGACGACCCGAGCACCGAGGCCGCGATCGACGCCCTGGACCCG
                                                                                        GGCATTICGACCGGCGCCTTCTACCCGGCCGCCGCCGGCCGCCCACCGAAGAGATCATC
                                                                                                                              GTCGCCCCCCTGCTCGTCGCCGAGCGCGCCACCGAGGCCGCCGTCGCCGACCTCGCC
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Pred. No. 0.00033;
0; Mismatches 749; Indels
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                                                           NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 6160
LENGTH: 1371
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                                                                                                                                                                                   FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                            PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                       ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                             RPPLICANT:
                                                                                                                                                                                                                                                                                                                                           APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
NAME/KEY: CDS
                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                              MERAL INFORMATION:
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                                                                                                                                                                                                                       NT: IKEDA, HARUO
NT: ISHIKAWA, JUN
NT: HORIKAWA, HIROSHI
NT: SHIBA, TADAYOSHI
NT: SAKAKI, YOSHITUKI
NT: HATTORI, MASAHIRA
DF INVENTION: NOVEL POLYNUCLEOTIDES
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RESULT 15
US-10-314-657-1/c
, Sequence 1, Application US/10314657
; GENERAL INFORMATION:
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TITLE OF INVENTION: DISCrete Acyltransferases Associated with Type I Polyketide ITITLE OF INVENTION: Synthases and Methods of Use FILLE REFERENCE: 054030-0021
CURRENT APPLICATION NUMBER: US/10/314,657
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: PCT/US02/08937
PRIOR APPLICATION NUMBER: BCT/US02/08937
PRIOR APPLICATION NUMBER: US 60/278,935
PRIOR APPLICATION NUMBER: US 60/278,935
PRIOR APPLICATION NUMBER: US 60/278,935
NUMBER OF SEQ ID NOS: 214
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APPLICANT: CHENG, Y1-Q1a
APPLICANT: TANG, Gong-Li
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Best Local Similarity
Matches 309; Conserv
                                                                                                                                                                                                                                                                                                                                                      1341 CCACCT 1346
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Pred. No. 0.00035;
0; Mismatches 351;
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SEQ ID NO 1
LENGTH: 135638
TYPE: DNA
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Best Local Similarity 44.3%;
Matches 610; Conservative
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                                                                                                                          CACCGCCTCGGCGTTCCTCCATCCCCCGCTCGCCCCGCGCCCTGTTGGCCGCGATGCCCCG 117179
                                                                                                                                                                                              GGCCCGCGTGATCGGCGCCTACTCGGCCAGCCAGGCCAAGCCCGCCGTGACCATCGGCAC 117119
                                                                                      CTGGTGCAAGCCCTTCCCCGAACTGAGCGGGGGGGGGCGACCTGGATGAAGTCGCGGGCCGAGCG
                                                                                                                                                          GCCCGGCTCCACCATGCTCAAGCAGGACCGCGTGCTGCTGGCCGGACGCACCATCATCAC 953
                                                                                                                                                                                                                                  GCCGCTGATCGAGGCCGCCATGGCGCCAGGACGTCTCGCTGGACGCGTATCCCTACGT 893
                                                                                                                                                                                                                                                                    CGCGCTCATCGAGCACCATGCGGCGAGCACCGTCATGATGACCCCGGAACCTCGCCGTGCA 117296
                                                                                                                                                                                                                                                                                                  GGTGATCTCGCACCACAAGGTCATGGGCCCAGCCCCAATTTCGGCCGCCTCGCGCGAGACGCT.
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Search completed: May 11, 2003, 12:05:20 Job time: 935 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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APPLICANT: MORIGUCHI, MITSUAKI
APPLICANT: ISOBE, Kimiyasu
ITITLE OF INVENTION: TRANSFORMED MICROORGANISM AND PROFILE REFERENCE: 217301USOPCT
CURRENT APPLICATION NUMBER: US/10/009,782
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: PCT/PP00/03932
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 2
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; OTHER INFORMATION:
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Best Local Similarity 100.0%;
Matches 1758; Conservative 0
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GENERAL INFORMATION:
APPLICANT: TAKEUCHI, Ken-ichi
APPLICANT: KOIDE, Yoshinao
APPLICANT: HIROSE, Yoshihiko
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SEQ ID NO 1
SERGIH: 1758
TYPE: DNA
ORGANISM: Alcaligenes xylosoxydans subsp. xylosoxydans
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: HIROSE, Yoshihiko
: MORIGUCHI, Mitsuaki
: ISOBE, Kimiyasu
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Sequence 74, Appl
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Sequence 96, Appl
Sequence 96, Appl
Sequence 1, Appl
Sequence 1, Appl
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Sequence 8, Appl
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Db Qy		; LENGTH: 1473 ; TYPE: DNA ; ORGANISM: Alcaligenes ; FEATURE:
Db ,		NUMBER OF SEQ ID NOS: 4 SOFTWARE: Patent Ver. 2.1 SEQ ID NO 3
Qy Db		CORRENT FILING DATE: 2001-04-18 PRIOR APPLICATION NUMBER: PCT/GB99/03458 PRIOR FILING DATE: 1000-10-20
У	AMINOACIDS	TITLE OF INVENTION: AMINOACYLASE AND ITS USE IN THE PRODUCTION OF D- FILE REFERENCE: GJE-239
B 7		APPLICANT: Stephen John Clifford Taylor APPLICANT: Robert Christopher Brown
ag b	;	RESULT 2 US-99-807-788-3 Sequence 3, Application US/09807788
δ S		4
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dg Qg	0 0	OY 1681 TCGCAGGCCAGCGGCATCGCGGTCTCGAACCCTGTCCAAGGCCGAGCTGGGCCAGATCGCC 1740
D 4	0 0	1621
) b	öö	1561
S B 7	6 6	
0 0 4	ŏ ŏ	1441
B &	10 10	1381
Db Qy	30 80	1321
•	20	1261

GACGGCGTATGGAAGATGACCGGCCTGACCGCGCGCGCCTGCGCCTGTTCCCG	231	Dy Cy	
GGGGCACCTTCCCGGGGTGCTGGGGCACTATGCGGGCGACCTGGGCCTGTTCCCGC	1171 T	8 원	
GCCCGACCATGATCGGCTCCGACGGCCTGCCGCACGACGAGCGCCCGCATCCGCGCTTG 	1111 G	Д QУ	
GGCCGGCGCCATCTAC	024	ğ	·
GGCCGGCGCCATCTACTTCATGATGGACGAACCCGACGTGCAGCGCATCCTGGC	1051	Qγ	
!TGGATGAAGTCGCGGCCGAGCGCGGGAAATCCAAGTACGACGTGGTGCCCGAGCTGCAG 	991 C	B 8	
TIGGCCGGACGCACCATCATCACCTGGTGCAAGCCCTTCCCCGAACTGAGCGGGGGGGACGCAC	04	망	
GCTGGACGCBTATCATCATCACCTGGCCGGCTCCACCATGCTCAAGCAGGACCGCCGT	931 0	6 B	
TCGCTGGACGCGTATCCCTACGTGGCCGGCTCCACCATGCTCAAGCAGGACCGCGTGCTG	71	Qy	
TICGCCCGCTCGCGCAAACGCTGCCGCTGATCGAGCCGCCATGGCGCGCCAGGACGTC	784 T	₽ 5	
	24	문	
CCCACATGCGCGACGAACGCGAAGCACATCGTGGCCGCGCTGGAGAAATTTTTTTT	664 A 751 G	5 B	
CCACATGCGCGACGAAGGCGAGGACATCGTGGCCGCCGCTGGAGGAAACCTTCCGC	91	ρy	
ACCACCGAAGAGATCATCGAGGTGTGCCGGCCGCTGAGCGCGATGGCGGGATCTACG 	631	D Q	
	44	gg	
TGGCCAGCGGCGCATCGGCATTTCGACCGGCGCCTTCTACCCGCCGCCGCCGC	571	Qy	
TTGCAGCGCGCCCACCGACGAGGAAATCGCGGCCATGCGGGACCTGGCCGAGGAAG 	484	ğ . 22	
	424	Db	
CCGTCAACGCCGCTGTATGGTGGGCCATTCAACGCTGCGCCCCGCTCATCATGCCC	451	γQ	
SUPPRISON	364	B 2	
CCTGGCACGCTGGCGCACGCCAACCCGCCCGGCCCCCTGGA		₽ ₽	
CCGCTGGCGCACGCCAACCCCGCCCCCCTGGACCTGCTGGACGAA	331	Qy	
GACATGACGCCAAGATCTCGCAGGGCGTCACCACGGTGGTCACGGCAATTGCGGC	244	뮍	•
ACATGACGCCCAAGATCTCGCAGGGCGTCACCACGGTGGTCACGGGCAATTGCG	271	VΩ	
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 1847 ID NOS: 14342
LENGTH: 1479
TYPE: DNA
ORGANISM: KLebsiella pneumoniae
US-09-489-039A-1847
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Sequence 1847, Application:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709,2004001
FILE REFERENCE: 2709,2004001
536 AAATCGCGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCATCGGCATTT 595
                                            476 GCCATTCAACGCTGCGCGCGCGGGTCATGCCGGACTTGCAGCGCGCCGCCGACGAGG
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                       GTCACACCGCGCTGCGTAATAACCATATGGACGATCTGTTTCGTCCGGCGAACGAGACGG
                                                                     AGGCTTÄTGCCCATGCGGTGGAGGCGGCGCGACCGTCGCTGAATGTCGGCACGTTAATCG
                                                                                            CCGACTACCTGGACGCGTTGCGGGCCACGCCGGCGGCCGTCAACGCCGCCTGTATGGTGG
                                                                                                                    ACCCGCCCGCCCCCCTGGACCTGGACGACGAAGGCGGCTCTTACCGTTTCGAGCGCTTCG 415
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                                                                                                                                                                                                                                                                                 CGCACACCCGGGTCGACGTGTCGGGCCTGGTGGTCGCGCCCGGCTTCATCGACTCGCACA 238
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Pred. No. 3.4e-56;
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Sequence 35, Application US/60184777
GEMERAL INFORMATION:
APPLICANT: Hodgson, David M.
APPLICANT: Hincoln, Stephen E.
APPLICANT: Russo, Frank D.
APPLICANT: Spiro, Peter A.
APPLICANT: Banville, Steve C.
APPLICANT: Banville, Steve R.
APPLICANT: Bufour, Gerard E.
APPLICANT: Cohen, Howard J.

'n,

Jones, Anissa L. Jimmy Y. Greenawalt, Lila B.

Rosen, Bruce

Panzer, Scott F Roseberry, Ann M. Wright, Rachel J. Chen, Wensheng Liu, Tommy

Yap,

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RESULT 4
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                                  AACGACCGGCGGACGGCATTGAGGCGGTGATGGTCAACGGCGTGATGAGCT 1417
                                                       CCSACCTGGTGCTGTTTGACCCGCAGACGGTGCGCGATGTCGCCAGTTTCTCCGACCCGA
                                                                                          CCGACCTGGTGGTGTTCGACCCGGCCACGGTGGCCGATACCGCCACCTTCGAACACCCTA 1375
                                                                                                                                     GCCTGACCGCCGCGCGCTTCGGCCTGGCCGGGCGGCGGCAGCTGCAGGCCGGGTACTTCG 1315
                                                                                                                        GCTGTCGCCGCCTCCAGCTGGCGGGATCGCCGGGCTGGTGAAAATTGGCTACTTTG
                                                                                                                                                                    GCCACTATAGCCGCGACGAGCAGCTATTCCCGCTGACTACCGCGGTACACAAGATGACCG
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RESULT 5
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APPLICANT: Chalup, Michael S.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: HUMAN ENZYME MOLECULES
FILE REFERENCE: PT-0113 p
CURRENT APPLICATION NUMBER: US/60/184,777
CURRENT FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 1471
SOFTWARE: PERL Program
SEQ ID NO 35
LENGTH: 453
TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID No: 373369.1

US-60-184-777-35
CURRENT APPLICATION NUMBER: US/10/152,886
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 54
LENGTH: 5877
                                                                                                                                                                             Sequence 54, Application US/10152886 GENERAL INFORMATION:
                                                                                   FILE REFERENCE: 3011-30S
                                                                                                                                 APPLICANT: ECOPIA BIOSCIENCES INC.
APPLICANT: Farnet, Chris
APPLICANT: Staffa, Alfredo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.6%;
Best Local Similarity 56.0%;
Matches 253; Conservative
                                                                                       APPLICANT: Farnet, Chris
APPLICANT: Staffa, Alfredo
APPLICANT: ZEXOPOULOS, Emmanuel
TITLE OF INVENTION: GENES AND PROTEINS INVOLVED
TITLE OF INVENTION: STRUCTURES
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Pred. No. 4.2e-11;
0; Mismatches 199;
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Fong, Willy Tuen
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Query Match
Best Local Similarity
Matches 659; Conserv
                              1025
                                                                                                                                   3122
                                                                                                                                                                                          3062 AACTCGCCGACCTGCTGGACGAGTTGGCCCAGCAGTCACCGCAGGACACCCCGCCGCG
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AGTACGACGTGGTGCCCGACCTGCACCTGCCGCCGCCGCCATCTACTTCATGATGGACGAAC 1084
                                                  CCTTCCCCGAACTGAGCGGGCGCGACCTGGATGAAGTCGCGGCCGAGCGCGAAATCCA
                                                                                                                                                    CCATGCTCAAGCAGGACCGCGTGCTGCTGGCCGGACGCACCATCATCACCTGGTGCAAGC
                                                                                                                       CCGCCGCCGGCGTCGCCTGGGTGCGGCCCTTCCGGATCGACCTCACCGAGACCCCGC
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Pred. No. 0.0002;
0; Mismatches 832;
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RESULT 6
US-09-976-059-1
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SEQ ID NO 1
LENGTH: 88421
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/976,059
CURRENT FILING DATE: 2001-10-15
                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 34
                                                      NAME/KEY: misc_feature
LOCATION: (4038). (5048)
OTHER IMPORMATION: ORF 3; positive strandedness
NAME/KEY: misc_feature
                                                                                                                   NAME/KEY: misc_feature
LOCATION: (4038)..(5048)
OTHER INFORMATION: ORF 3; positive strandedness
                                                                                                                                                                              LOCATION: (3118)..(4032)
OTHER INFORMATION: ORF 2; positive strandedness
                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Actinoplanes sp
                                                                                                                                                                                                                                    LOCATION: (2077)...(3078)
OTHER INFORMATION: ORF 1; positive strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLICANT: Farnet, Chris
                                                                                                                                                                                                                         AME/KEY: misc
                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
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PPLICANT: Staffa, Alfredo
ITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE: 3019-PCT
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           ORF 4; negative strandedness
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               NAME/KEY: misc_feat
LOCATION: (82346)...
OTHER INFORMATION:
                                                                      LOCATION: (81909)..(81682)
OTHER INFORMATION: ORF 27;
                                                                                                                             OTHER INFORMATION: ORF 26;
                                                                                                                                                                                   LOCATION: (79864)..(78107)
OTHER INFORMATION: ORF 25;
                                                                                                                                                                                                                                          LOCATION: (78110)..(76449)
OTHER INFORMATION: ORF 24;
                                                                                                                                                                                                                                                                               NAME/KEY: misc
                                                                                                                                                                                                                                                                                                 LOCATION: (75535)..(76464)
OTHER INFORMATION: ORF 23;
                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: ORF 22;
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OTHER INFORMATION: ORF 21;
                                                                                                                                                                                                                             NAME/KEY: misc
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OTHER INFORMATION: ORF 20;
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LOCATION: (12751)..(10829)
OTHER INFORMATION: ORF 8;
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OTHER INFORMATION: ORF 19;
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THER INFORMATION: ORF 18;
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THER INFORMATION: ORF 17;
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OTHER INFORMATION: ORF 14;
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OTHER INFORMATION: ORF 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (15880)..(19035)
OTHER INFORMATION: ORF 12;
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THER INFORMATION: ORF 10;
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THER INFORMATION: ORF 6; negative strandedness
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OTHER INFORMATION: ORF 5; negative strandedness
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THER INFORMATION: ORF 9; negative strandedness
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LOCATION: (8555)..(86845)
OTHER INFORMATION: ORF 31; p
NAME/KEY: misc_feature
LOCATION: (87372)..(86803)
OTHER INFORMATION: ORF 32; p
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LOCATION: (87494)..(88420)
OTHER INFORMATION: ORF 33;
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LOCATION: (84481)..(85548)
OTHER INFORMATION: ORF 30;
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ATTTCGGCCGCTCGCGCGAGACGCTGCCGCTGATCGAGGCCCCCATGGCGCGCCAGGACG
                                                                                                                                    CCACCCACATGCGCGACGAAGGCGAGCACATCGTGGCCGCGCTGGAGGAAAACCTTCCGCA
                                            TCTTCGTCAACACGCTCGTGCTGCGCACCGACCTGACCGGCGACCCGGCGGCTGACCGACG
                                                                         TCGGCCGCGAGCTGGACGTGCCGGTGGTGATCTCGCACCACAAGGTCATGGGCCAGCCCA
                                                                                                       TCCCGATCGGCACCGTCGTCGCCGGCCGCGCCGACCGGGCGCTGGAGAACCTGGTCGGCT
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Pred. No. 0.00037;
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US-09-739-449-925
Sequence 925, Application US/09739449
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens
FILE REFERENCE: 38-10(15990)C
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                                                                                                                                       ; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(770)
; OTHER INFORMATION: unsure at all n locations
US-09-739-449-925
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Best Local
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PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 925
LENGTH: 770
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US CURRENT FILING DATE: 2000-12-
                                                                                                                                                                                                                               ORGANISM: Agrobacterium tumefaciens
                             1078 GACGAACCCGACGTGCAGCGCATCCTGGCCGTTCGGCCCGACCATGATCGGCTCCGACGGC 1137
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                                                                                        Local Similarity
CCGATACCGCCACCTTCGAACACCCTACCGAGCGCGCCGCCGGCATCCATTCCGTGTACG
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                                                                                      Score 85.4; DB 29; Pred. No. 0.00089;
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: LOCATION: (1)..(770)
: OTHER INFORMATION: unsure at all n locations
US-09-803-110-925
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Best Local Similarity
Matches 214; Conserv
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GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof CURRENT APPLICATION NUMBER: US/09/803,110
CURRENT FILING DATE: 2001-03-12
PRIOR REPLICATION NUMBER: """
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 09/514,000 PRIOR FILING DATE: 2000-02-23 PRIOR APPLICATION NUMBER: US 60/168,139 PRIOR FILING DATE: 1999-12-01 NUMBER OF SEQ ID NOS: 13351 SEQ ID NO 925 LENGTH: 770
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/739,449
PRIOR FILING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                        ORGANISM: Agrobacterium tumefaciens
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                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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                        CTGACCGCGCGCTTCGGCCTGGCCGGGCGGGCAGCTGCAGGCCGGGTACTTCGCC
                                                 CTGCCGCACGACGAGCGCCCATCGGCGCCTGTGGGGCACCTTCCCGCGGGGTGCTGGGG 1197
                                                                         CACTATGCGCGCGACCTGGGCCTGTTCCCGCTGGAGACGGCGGTATGGAAGATGACCGGC 125
GAGCGCCCCCCCGCCATCCATTCCGTGTACGTCAACGGCGCCGGCCTCTGGCAAGAGCAG 1437
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                                                                                                                                                                                                                       Score 85.4;
Pred. No. 0
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Mismatches 205;
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; ORGANISM: Micromonospora carbonacea
US-09-758-759-1
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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Best Local Similarity
Matches 542; Conserv
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TITLE OF INVENTION: Everninomicin Biosynthetic
FILE REFERENCE: ID0983K US
CURRENT APPLICATION NUMBER: US/09/758,759
CURRENT FILING DATE: 2001-01-11
                                                                                                                            94858
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CCTGGACCTGCCGGCCGGCCGGGTCGCCGTGGTCGGGCCGAGCGGCGCCGGCAAGAG
                           CATCGGCATTTCGACCGGCGCCTTCTACCCGCCCGCCGCCGCCGCCACCACCAAGAGAT 644
                                                         CTTCGACGCGGTCACCGGGTACCGGGCCGGCACCGGCCCCGGGCCCTGGACCGGGTCAC
                                                                                   CACCGACGAGGAAATCGCGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGC
                                                                                                                  CGCCACCCGCCGGTGCCGCGTGCCGTCGGTGCCGGCCGCACGACGTGCG
                                                                                                                                             CTGTATGGTGGGCCATTCAACGCTGCGCGCGCGGTCATGCCGGACTTGCAGCGCGCCGC
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US-09-758-759-150

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APPLICANT: Hosted, Thomas J.
APPLICANT: Wang, Tim X.
APPLICANT: Horan, Ann C.
ITILE OF INVENTION: Everninomicin Biosynthetic Genes
FILE REFERENCE: ID0983K US
CURRENT APPLICATION NUMBER: US/09/758,759
CURRENT FILING DATE: 2001-01-11
FRIOR APPLICATION NUMBER: US 60/175,751
PRIOR APPLICATION NUMBER: US 60/175,751
PRIOR FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 204
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 150
LENGTH: 1839
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                                                                                                                                                                                                                                                                                        Sequence 150, Application US/09758759 GENERAL INFORMATION:
NAME/KEY: CDS
LOCATION: (1)..(1839)
OTHER INFORMATION: evcE
                                                  ORGANISM: Micromonospora carbonacea FEATURE:
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Local Similarity 45.6%;
les 515; Conservation
GGCGGCGACCCCGCGGGCACTCGGTGCTGCTGATCAGCCACCGGCTCAGCGGGCTCGC
                          GCAGCCGGCCGCCGCCATCTACTTCATGATGGACGAACCCGACGTGCAGCGCATCCTGGC 1106
                                                                                  GGATGAAGTCGCGGCCGAGCGCGCAAATCCAAGTACGACGTGGTGCCCGA-----GCT 1046
                                                                                                                                           CCGGACGCACCATCATCACCTGGTGCAAGCCCT--TCCCCGAACTGAGCGGGCGCGACCT
                                                       CGACGAGCCGACGGGGGCTCGACCCGTCCGCCGACGCGGTGCTCGCCTCGGCGCT
                                                                                                                 CCAGCGGCAGCGCTCGCGCTGGCCCGGGCGCTGCTCGCCGGGGTGCTGGTGCT
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Pred. No. 0.0013;
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GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF
TITLE OF INVENTION: LEINAMYCIN BIOSYNTHESIS
FILE REFERENCE: 3997-000110PC
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NUMBER OF SEQ ID NOS: 222
SOFTWARE: PatentIn version 3.0
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CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US 60/278,935
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ORGANISM: Streptomyces atroclivaceus
                                                                                                                                                                           537 AATCGCGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGACCATCGGCATTTC 596
                                                                                                                                                                                                                                                                                                                                           417
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Local Similarity 44.3%;
ues 610; Conserva+...
CCCCATGGTGGCGTCCGTGAACCTGGGCATCACCGCGAGCGCCACCACCGTCTCCATGGT 117416
                                 CC---GGCCGCTGAGCGCGCATGGCGGCATCTACGCCACCCACATGCGGCGACGAAGGCGA 713
                                                                    GCACCAGAACCTCGCGACGGCGGGCGGACCGCCCTCCGTGATGGCGCACGACGACGCCCAC 117476
                                                                                                        CGCCGCGAGATCGTGTACTCCTCCGGCACCACCGGACTGGCCCGCGGCGTCGTCGTCTC
                                                                                                                                                                                                                                                CCATTCAACGCTGCGGCGCGGGTCATGCCGGACTTGCAGCGCGCCGCCGACGAGGA 536
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                                                                                                                                                                                                                                                                                                                       CGACTACCTGGACGCGTTGCGGGCCACGCCGGCGGCGGTCAACGCCGCCTGTATGGTGGG
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Pred. No. 0.001
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NUMBER OF SEQ ID NOS: SOFTWARE: FastSEQ for SEQ ID NO 7

for Windows Version

ENGTH: 1248

ORGANISM: Streptomyces

venezuelae

APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin
FILE REFERENCE: 600, 438US1
CURRENT APPLICATION NUMBER: US/09/836,821
CURRENT FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26

and pikromycin

Sequence 7, Application US/09836821

GENERAL INFORMATION:

APPLICANT: Sherman, D.H. APPLICANT: Liu, H.

APPLICANT:

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US-09-836-821-7
                                                  Db 116701 GETGGEGGECACCETEGECGETEACGEGAAGGAEAGETEGGECECECAEGAGATECEC 116644
                                                                                                                                                                                                                                                                                Db 116878 CTTCGACCCCAGACCGACGCCGTGCCCACACCGGCCTGGTCGTCGTCCTCCTG---CG
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                                                                                                                                                                                                      GGTCGAGTCGGTCCTGCTCGAGCACGAGGCGGTCGCCGACGCGGCCGTGGTCGCCGCCGG 116762
                                                                                           GCCGGCCGGCGTGGCCGCGATCGTGCCCGCGGCCGCGCGCACCCATGACCCGAAGCT 116702
                                                                                                                                                                                                                                     GTACTTCGCCGACCTGGTGGTGTTCGACCCGGCCACGGTGGCCGATACCGCCACCTTCGA 1367
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; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-860-846-7
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Best Local Similarity
Matches 439; Conserv
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GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
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CURRENT APPLICATION NUMBER: US/09/860;846
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
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                                 CCGCCTACCGCGAGCACCTCGCGGACCTCCCCGGCGTCCTCGTCGCCGACCACGACCGCC
                                                                CCACCGAAGAGATCATCGAGGTGTGCCGGCCGCTGAGCGCGCATGGCGGCATCTACGCCA
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Pred. No. 0.003;
0; Mismatches 542;
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US-09-861-289-7
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 7
LENGTH: 1248
TYPE: DNA
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CURRENT APPLICATION NUMBER: US/09/861,289
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
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ACATGACGCCCAAGATCTCGCAGGGCGTCACCACGGTGGTCACGGGCAATTGCGGCATCA 331
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; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-988-384B-7
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                                                                                                                                                           CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: PCT/US99/14398
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,537
PRIOR FILING DATE: 1998-06-26
                                                                                                                                                                                                                  TITLE OF INVENTION: DNA encoding methymycin FILE REFERENCE: 600.536US1
CURRENT APPLICATION NUMBER: US/09/988,384B
CURRENT FILING DATE: 2001-11-19
                                                                                                                                                                                                                                                                                                    APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
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Score 81.8; DB 37; Pred. No. 0.003; Mismatches

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Search completed: May 11, 2003, 11:55:40 Job time : 3920 secs

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AAZ87318	AAZ87297	AAS51474	AAD14499	AAQ91580	AAD14501	AAZ32022	AAC90079	AAV10362	AAV68520	AAZ87283	AAT68715	AAQ22485	AAQ22484	AAQ22482	AAN92408	AAT80413	AAT91361	AAA58471	AAT06769	AAQ76213	AAZ56003	AAA75635	AAD25519	AAD25519	AAC55857	AAC55840	ABADGERE	AA022481	EVUDELLE	AAZ87319	AAZ87284	AAD39044	AAZ87286	AAS08693	AAL40781
venezuelae pik	S. venezuelae macr	Pseudomonas aerugi	#	S. Clavuliderus cl	ω.	ETH1	L05390 cDNA clone.	Infected cell prot	The nucleotide sec	S. venezuelae vep	ξ.	groek-1 gene str	gro es el oneron w	groek-1 gene codin	Sequence encoding	Tylactone synthase	Orf virus genomic	Nucleotide sequenc	Spranging cellulos	HSV I./ST TEATON CO	Contig DOS from co	Nicleotide sector	Human hernesylvus	complete defined	Complete micomycin	Complete With the Complete Com		omyces	. venezuetae		rrepromyces v		or jensenen	A CARATIC RECORDS	2000

ALIGNMENTS

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WPI; 2001-080828/09. P-PSDB; AAB48975.	Takeuchi K, Koide Y, Hirose Y, Moriguchi M, Isobe K;	(AMAN-) AMANO ENZYME INC.	17-JUN-1999; 99JP-0170555.	15-JUN-2000; 2000WO-JP03932.	28-DEC-2000.	W0200078926-A1.	Alcaligenes xylosoxidans.	ds.	D-aminoacylase; zinc tolerant host; recombinant production; zinc-enhanced expression; D-form amino acid synthesis;	Alcaligenes xylosoxidans subspecies xylosoxidans D-aminoacylase DNA.	27-MAR-2001 (first entry)	AAC91797;	RESULT 1 AAC91797 ID AAC91797 standard; DNA; 1758 BP.

Claim

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Sequence 1758

61 61

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Query Match
Best Local Similarity
Matches 1758; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a recombinant zinc-tolerant microorganism which expresses the D-aminoacylase from Alcaligenes xylosoxidans subspecies xylosoxidans. The presence of zinc ions in the culture medium enhances the process of recombinantly producing the Invention also relates to microorganism of the invention. The recombinant microorganism is used for the selective production of D-aminoacylase, which is useful in the production of high optical-purity D-form amino acids for use in the production of antibiotics and peptide drugs. The present sequence subspecies xylosoxidans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transformed microorganism from zinc-tolerant host for selective production of D-aminoacylase, useful in synthesis of high optical-purity D-amino-acids for antibiotic side-chains and pepidrugs -
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                                                                          GCGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCCATCGGCATTTCGACC
                                                                                                                                 TCAACGCTGCGCGCGCGTCATGCCGGACTTGCAGCGCGCCGCCCACCGACGAAGGAAATC
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                                                                                                                                                                   CCCGCCCCCTGGACCTGCTGGACGAAGGCGGCTCTTACCGTTTCGAGCGCTTCGCCGAC
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            CTGAGCTACGAGAAGCTT
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                                       TCGCAGGCCAGCGGCATCGCGGTCTCGACCCTGTCCAAGGCCGAGCTGGGCCAGATCGCCCTGTCTCTAAGGCCGAGCTGGGCCAGATCGCCC
                                                             TCGCAGGCCAGCGGCATCGCGGTCTCGACCCTGTCCAAGGCCGAGCTGGGCCAGATCGCC
                                                                     GTGATGGGCGCGCGCGTGCGCGCGAGCGCGAAGGGCCCGGAAAATGACCCTGCAAGACCTG
                                                                                                      CGCTACATGGCCCCTCCCTCCGCTCGCCAATACGGCCCCACCCGATATCGTCGGCCAAGGAA
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Best Local Similarity
Matches 1449; Conserv
                                                                                                                                                                                      The present sequence encodes an aminocyclase enzyme. The enzyme is capable of hydrolysing N-acetyl-D-tryptophan at a substrate concentration of 10 grams per litre, and exhibiting faster convers of R-N-acetyl-2-thienylalanine than of R-N-acetyl-2-thienylalanine than of R-N-acetyl-4-chlorophenylalanine. The enzyme can be used for the preparation of a D-amino acid by conversion of a corresponding D-N-acylamino acid. It can also be used for resolving a racemic mixture of N-acylamino acids and deprotecting optically-enriched the production of various pesticides, antibiotics and other
                                                                                                                                                                                                                                                                                                          New isolated D-amino acylase enzyme, useful for the preparation D-amino acids for use as intermediates in the preparation of pesticides, antibiotics and other pharmaceuticals
                                                                                                                                                                    Sequence 1473 BP;
                       124
                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                   20-OCT-1998;
01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aminocyclase; N-acetyl-D-tryptophan; R-N-acetyl-2-thienylalanine; R-N-acetyl-4-chlorophenylalanine; D-amino acid; N-acyl amino acid; pesticide; antibiotic; ss.
                                                                                                                                                                                                                                                                                                                                                                                              (CHIR-) CHIROTECH TECHNOLOGY LTD.
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                 GACGGCAGCAACACCCCGGGGCGGGCGCGCGACCTGGGCGTGCGCGCGACCGGACCGCATCGCC
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99GB-0007739.
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GGGCAGCTGCAGGCCGGGTACTTCGCCGACCTGGTGGTGTTCGACCCGGCCACGGTGGCC
                 TGGGGCACCTTCCCGCGGGTGCTGGGGCACTATGCGCGGGACCTGGGCCTGTTCCCGCTG
                                                                                       GGCCCGACCATGATCGGCTCCGACGGCCTGCCGCACGACGACGCGCCGCCATCCGCGCCTG
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483 570 390 363 450 423

1230 1203 1290 1170 1143 1083 1110 1023 1050 963 .90 903 930 843 870 783 810 723 750 663 690 603 630 543

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The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the regions and all segments of RNAs exection between coding and non-coding or more diseases, conditions or mixtures. The antisense oligonucleotides (specifically AAX55272-74. These multiple target antisense treatment of diseases and conditions. Typical diseases and inflammation, including lung diseases, pulmonary vasoconstriction, including lung diseases, pulmonary vasoconstriction, impedeed antisense conditions.
                                                                                                                                                                                                                  Disclosure; Page 37; 120pp; English.
                                                                                                                                                                                                                                            New antisense oligonucleotides used in treatment of, e.g. pulmonary vasoconstriction
                                                                                                                                                                                                                                                                                                  WPI; 1999-229400/19
                                                                                                                                                                                                                                                                                                                                                                                          09-JUN-1998;
17-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                             (UYEC-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9913886-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 ACG--CCGCCGCGCACACCCGGGTCGACGTGTCGGGCCTGGTGGTCGCGCCCGGCTTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or have metastasized to the lungs, including breast and prostate cancer
CGCCCVGGCCVGCGGNNHNNNSC----CGGCCGGCGCGCGCCCVGGCCVGCGGNNHNNNS 104377
                                                                                     GCCVGCGGNNHNNNSGGCCGGCGGCGCGCCCVGGCCGGCGGNNHNNNSCGGCCGGCGGCG
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                                                                                                                                                                                                                                                                                     Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythema
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                                                                                                                                                                                                             autoimmune disorder; rheumatoid arthritis;
                                                                                                                                                                                                                                    hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUN-2002 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABN24790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABN24790 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNNSGCCCGGCCGACGCCAVGACGGCNNHNNNSGCCCGGCCCGACGCCGCCAVGAC
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                                                                                                                                                                                                       thyroiditis;
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TCGGCCGCGAGCTGGACGTGCTGGTGATCTCGCACCACAAGGTCATGGGCCAGCCCA 808

TCGGCAAACATGCGCGCGTGCCGGTGGTGATCTCACACCTGAAATGCGCAGGCGCTGCCA 181

CCACCCACATGCGCGACGAAGGCGAGCACATCGTGGCCGCGCTGGAGGAAACCTTCCGCA 748 CGACCACCGAAGAAGTGATGGGCCTGGCGGAGCCGCTGGCCGAAGCTGGCGGGTCTACA 61

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TGGGTTGCGACTGCTATCCGTACACCGCAAGCTCGTCCACGCTGGACCTCAAGCAGGTG TCTCGCTGGACGCGTATCCCTACGTGGCCGGCTCCACCATGCTCAAGGACGGCGCGTG 927

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ATTTCGGCCGCTCGCGCGAGACGCTGCCGCTGATCGAGGCCGCCATGGCGCCCAGGACG

ATTGGGGCCGCGGGCGAGGTGCTGGAATCCATCGAAGGTGCACAGTGCTATCAGCCGG

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                                                Matches 175;
                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                          lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and diseases, rheumatoid stresses, autoimmune disorders such as multiple scierosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. OREX proteins are also meefin for the third inflammatory eye disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (referred to as open reading frame, ORFX, where X is 1-11491 [See Table in the specification). ABM15762 to ABM27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrbosis of liver, osteoarthritis, neurodegenerative disorders, disorders related to organ representatives.
                                                                                                                         Sequence 312 BP; 62 A; 92 C; 105 G; 52 T; 1 other;
                                                                                                                                                                                  N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                 reperfusion injury in various tissues and conditions resulting systemic cytokine damage.
                                                                                                                                                                                                                                                               useful for treating burns, incisions, ulcers, for treating osteoporosis bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis,
629 CCACCACCGAAGAGATCATCGAGGTGTGCCGGCCGCTGAGCGCGCATGGCGGCATCTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                              transplantation, cardiovascular diseases, diabetes mellitus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID 18057; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000;
29-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAY-2001;
                                                                      Local
                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention
                                                                    Similarity
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                                                Conservative
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2000US-228716P.
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                                            0;
                                                               Score 101.2;
Pred. No. 1.6
                                            Mismatches 124;
                                                               1.6e-07
                                                                                  DB 24;
                                          Indels
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AAD17184
ID AAD1
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AC AAD1
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KW Poly
KW Poly
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(UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
(SNTF) SINTEF STIFTELSEN IND TEK FORSK.
(ALPH-) ALPHARMA AS.
                                                                  08-FEB-2000;
10-APR-2000;
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                                                                                                                         16-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polyketide synthase; PKS; macrolide; nystatin; PKS gene cluster; antifungal; antibiotic; nysl; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces noursel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD17184;
                                                 2000GB-0002840.
2000GB-0008786.
2000GB-0009387.
                                                                                                2001WO-GB00509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            noursei nysl DNA of nystatin PKS gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                           /note= "CDS does not 63765..64961
                                                                                                                                                                                                                                  /product= "NysR5 protein"
/note= "CDS does not include
complement (62551..63615)
                                                                                                                                                                /product= "ORF1 protein"
                                                                                                                                                                                                             'product "ORF2 protein"
                                                                                                                                                                                                                                                                                          'product= "NysR4 (short) protein"
note= "CDS does not include start codon"
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duct= "NysRl protein"
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e= "CDS does not include stop
lement (1056..2576)
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uct= "NysB protein"
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662 CGCTGAGCGCGCATGGCGGCATCTACGCCACCCACATGCGCGACGAAGGCGAGCACATCG
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                                                                                                                                                                                                                                                                                                                            302 CCACGGTGGTCACGGGCAATTGCGGCATCAGCCTGGCGCCGCTGGCGCCAACGCCAACCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to the cloning and sequencing of the cluster encoding a modular type I polyketide synthase (PKS) enzyme involved in the biosynthesis of the macrolide antibiotic nystatin. The nystatin PKS is useful as antifungal antibiotics. The present sequence is a Streptomyces noursel nysl DNA of nystatin PKS gene c.
                                                                                                                                                                                                                                                                                                                                                                                                242
                                                                                                                                                                                                                                                                                                                                                                                                                                                     182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 65140 BP; 8270 A; 25171 C; 22273 G; 9426 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 ACCTGGGCGTGCGCGGCGACCGCATCGCCGCCATCGGCGATCTGTCGGACGCCGCCGCGCGC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nystatin polyketide synthase polynucleotides and polypeptides, useful as antibiotics and antifungals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-557614/62.
P-BSDB; AAE10125, AAE10126, AAE10127, AAE10128, A
AAE10131, AAE10132, AAE10133, AAE10134, AAE10135,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zotchev
Valla S
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                         CCGCCCCCGCGACCTGGCCGCCTCGCCGACGCCGAAGGGCCCGTCCCCGACCTGGTCG
                                                    GCGCCTTCTACCCGCCGCGCGCCGCGCGCCACCGAAGAGATCATCGAGGTGTGCCGGC
                                                                              TCCTCGGCCCGACCCGGACGCCCTCGCCGACACCCTCCGCGCCACCGGCATCCGGACCA
                                                                                                        CGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGGGGCGCCATCGGCATTTCGACCG
                                                                                                                                    TCCACGTCGAGTGGACCCCGCTCCAGGGCCGCCCGGGCCCCGCACCGGCCACCGTCGCCG
                                                                                                                                                            CAACGCTGCGCGCGGGTCATGCCGGACTTGCAGCGCGCCGCCACCGACGAGGAAATCG
                                                                                                                                                                                         CCCGCGAGGTCCCCGCCGACGCÀCCCGGCGCGCGCCGGCACCGTCCACCGCGACTCCCTCT
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                                                                                                                                                                                                                                                                       CCGCCCCCTGGACCTGCTGGACGAAGGCGGCTCTTACCGTTTCGAGCGCTTCGCCGACT 421
                                                                                                                                                                                                                                                                                                 TOSCOGCOGCOGCOCACCACCGTCCGCGCCCGGATCGCCCCGGGCGAGGACACCG 19997
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S, Ellingsen
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FJAERVIK E.
BRAUTASET T.
STROM A R.
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DZIEGLEWSKA I
ZOTCHEV S B.
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lingsen TE,
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43.58;
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E, Sletta H,
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Pred. No. 1.8e-07;
0; Mismatches 913;
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5, AAE10136, AAE10137.
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RESULT

New nystatin polyketide synthase polynucleotides and polypeptides, useful as antibiotics and antifungals -

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WPI; 2001-557614/62.
P-PSDB; AAE10143, AAE10144,
                                                                                                                                                                                           08-FEB-2000; 2000GB-0002840.
10-APR-2000; 2000GB-0008786.
14-APR-2000; 2000GB-0009387.
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                                                                                           DZIEGLEWSKA H.

ZOTCHEV S B.

SEKUROVA O N.

FJAERVIK E.

BRAUTASET T.

STROM A R.
                                                                  SB, Sekurova O
Ellingsen TE,
                                                                                                                                                                 UNIV NORGES TEKNISK NATURVITENSKAPELIGE SINTEF STIFTELSEN IND TEK FORSK.
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20628..121308
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note= "CDS does not include
note= mot (60238..61296)
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155..57355
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letta H, Gulliksen O;
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        CCGACACCGGCCGGGCCCGACCCCTGGC---
                          CCACCATGCTCAAGCAGGACCGCGTGCTGCTGGCCGGACGCACCATCATCACCTGGTGCA 961
                                                     GCCTGATCCGCACCGCCCCCCAGAGAACCCCGGCCGTTTCGCCCTCCTCGACCTCGCCC
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Pred. No. 1.7e-07;
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--CACCGCCCTGGCCGCCAGCC 80852
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                                                                              attenuated virus; vaccine;
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                                                                          Pseudorabies virus; PRV; LLV; large latency attenuated virus; vaccine; early protein 0;
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                                                                     protecting
                                                                                                            DNA encoding Pseudorables virus large latency transcript.
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                                                                 animals; deletion
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EPO; HSV-1
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Location/Qualifiers 1..7013

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                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                               AAQ73500 shows the Pseudorables virus (PRV) large latency transcript (LLT). The basic sequence is derived from PRV strain Infh and PRV strain Ka. The LLT overlaps and is transcribed in the opposite orientation with respect to the EPO (early polypeptide 0) and the immediately early gene (IE180). EPO is nonessential for replicatio, LTT is the only gene expressed during PRV latency, and the IE180 gene is absolutely necessary for PRV replication. However there are 2 copies of IE180 in the genome. It is expected that PRV lacking one of the IE180 copies is viable. Deletions in the non-overlapping regions of these 3 genes will generate single deletion routants, while deletions in overlapping regions will generate double deletion
                                                   5484
                                                                                                                                                                5604
                                                                                                                                                                                                                                                                                             mutants. The invention is concerned with the construction of attenuated viruses which have a reduced ability to reactivate from latency. This can be achieved by functionally disabling the expression of the EPO gene, or by disrupting the synthesis of the LLT, or both (See also AAQ73501 and AAR60620-24)
                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Column 15-30; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New pseudorables virus mutants for use in vaccine -deletion and/or insertion in the early protein O ger latency transcript gene
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es 608; Conser
GTCGCGCCCGGCTTCATCGACTCGCACACCACGACGACGACAACTACCTGCTCAGGCGTCGC
                                          GCCATCGGCGATCTGTCGGACGCCGCCGCGCACACCCCGGGTCGACGTGTCGGGCCTGGTG
                                                                                                 CGCGCCGGCCCACCGTCTCCGCCGCGCGCGCGCGCGCCGCGCGCCTCCGCCTCCC
                                                                                                                                                        TCCTCGTCCTCCGAGGGAGAAGAAGAAGAAGAAGGAGTCCGGCCCGGCGCCCCCACTCGCC 5545
                                                                                                                           TCCATGTCCCAATCCGATTCCCAGCCCTTCGACCTGCTGCTCGCGGGGGGGCACCCTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AK,
                                                                                                                                                                                                                                                                          8438 BP;
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Pred. No. 1.
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GAGCCCGCGCCCGGCCTGCCCCCCCCCCGAGCAGCCCGGCCTCGTCGTCCCAGCG
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                                                                                            CC The specification describes antisense oligonucleotides (AAX52869-X55271) CC directed against at least 2 mRNAs selected from target genes, coding and CC initiation codons, genomic flanking regions, intron-exon borders, the CC s'-end, the 3'-end and the juxta-section between coding and non-coding CC or more diseases, conditions or mixtures. The antisense oligonucleotides conditions or mixtures. The antisense oligonucleotides (specifically AAX55272-74. These multiple target CC antisense treatment of diseases and conditions. Typical diseases and CC disjonucleotides (specifically AAX55280-271) can be used for the CC conditions are those associated with impaired respiration and conditions are those associated with impaired respiration and CC inflammation, including lung diseases, pulmonary vasoconstriction, cc respiration, respiratory diseases, pulmonary vasoconstriction, cc pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic constructive pulmonary disease (COPD), and cancers such as leukemias, carcinomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, cc hepatic metastases, as well as all types of cancers, melanoma, carcinoma, kidney cancer, melanoma, cc or have metastasized to the luncs. Including breast and progratate cancer.
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pulmonary vasoconstriction; inflammation; allergic rhinitis;
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                                                                                                                                                                                                                       complement (454..1191)
                                                'product= "NysI partial protein"
                                                                                                                                                                                                                                ocation/Qualifiers
                                                                      product= "NysD3 protein"
338..27541
                                                                                                                                                                                       product= "NysF protein"
                                                                                                            note= "CDS does not include
product= "NysH protein"
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Valla S
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10-APR-2000;
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CGTCAGGACGACGCGACCGCGGCCTGGGCAGCCGACGTCGAGACCGCCCTGGGCACCACC 24028
                                                                                                                CAGACCGAACTGGACTCCTGGCGCTAC---CGCGTCACCTGGAAGCCGCGCGGCGGCGCCC
                                                                                                                                           CTGGACGAAGGCGCTCTTACCGTTTCGAGCGCTTCGCCGACTACCTGGACGCGTTGCGG
                            GTCATGCCGGACTTGCAGCGCGCCGCCACCGACGAGGAAATCGCGGCCATGCGGGACCTG
                                                         ACCGCACCCGCCCCTCACCGGCCGCTGGCTCGTGCTCCCGCACGACCACCAGGAC
                                                                                    GCCACGCGGCGGCGTCAACGCCGCCTGTATGGTGGGCCATTCAACGCTGCGCGCCGCG
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ZOTCHEV S B.

SEKUROVA O N.

FJAERVIK E.

BRAUTASET T.

STROM A R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SB, Sekurova ON,
Ellingsen TE, (
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2000GB-0008786
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Pred. No. 1.6e-06;
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Gulliksen O;
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                                                                                                           GGCGTGAACGGGGGGGGGGGGGCGCCCCCCCCCAACCCCTGGACGCAAACCGC 1563
                                                                                                                                                                                                                GTGCTGCGCCCAAGACCGTCGCCGCCCACCACCTGCACGAGCTGACCGCCGACCTGGAC
                                                                               GCAACTACGCGGGGCCAACGCCCACCTGGACGCCTCGCCGAACACCGC
                                                                                                                                              CTCGCCGCTTTCGTGCTGTTCTCCTCCACGGCCGCGCGTCCTCGGCGCGCCGGACAG---
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(first entry)

88421nt genomic DNA of ramoplanin producing Actinoplanes

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Ramoplanin; ramoplanin biosynthetic pathway polypeptide; antibiotic; biosynthesis gene cluster; bioengineering; peptide synthetase module; adenylation domain; hydroxyphenylglycine; HPG; antibiotic precursor; chlorinate; lipdepsipeptide; gene; ds.

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12-APR-2001;
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                                                                                   Novel isolated ramoplanin biosynthetic pathway chemically modifying biological molecule that j polypeptide encoded by a ramoplanin biosynthesj
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밁 Š 맑 Š 밁 Ş 몂 Ş 밁 S 밁 Š 20 밁 밁 Š 맑 맑 Ş Š CC modifies the biological molecule. The method comprises contacting the CC biological molecule with at least two different polypeptides encoded by CC ramoplanin ORFS 1-31. The polypeptides are useful for directing the CC biosynthesis of the antibiotic ramoplanin in microorganisms. An isolated CC gene cluster comprising the ORFS is useful as substrate for CC encoding nucleic acid sequence is useful as substrate for CC encoding nucleic acid sequence is useful for generating derivatives of CC ramoplanin, for improving production or for producing variants of other CC antibiotics of the peptide class. The isolated polypeptides are useful CC in conjunction with other peptide synthesis and allowing the CC incorporation of Thr into a peptide antibiotic precursor, for modifying the CC incorporation of Thr into a peptide antibiotic precursor, for enhancing the CC incorporation of Thr into a peptide antibiotic, for enhancing secretion of CC peptide antibiotic structure, for production of an hydroxyphenylglycine CC encodining peptide antibiotic, for enhancing useretion of CC production of its variants and derivatives, for enhancing production of CC ramoplanin products or its variants or derivatives, to chlorinate HPG of CC peptide antibiotic precursor, and for designing specific nucleotide probes and primers for identifying and isolating putative lipdepsipeptide CC producing microorganisms. This polynucleotide sequence represents the CC ability genomic DNA of a ramoplanin producing Actinoplanes sp: microorganism of the invention. Query Match Best Local Matches 46530 46470 46410 46350 46290 46230 629 Sequence 88421 BP; 10639 A; 32391 C; 32663 G; 12728 T; 0 other; 449 329 215 155 molecule with the isolated polypeptide, modifies the biological molecule. The me 95 35 Local CCACCAACGAAGAGATCATCGAGGTGTGCCGGCGCGCGGAGGGCGCATGGCGGCATCTACG TCCCGGCCGACGTGCACCGGAGCCTGCGCCGGGTCGCCGACCACGGCGCGACCGTCT CCGCCGACCGGCCGCGCGCCGCGCGCCTCGCACCGCGGCCACCTGCACAGGCGCGGAGA 46769 ACTTGCAGCGCGCCGCCACCGACGAGGAAATCGCGGCCATGCGGGACCTGGCCGAGGAAG ACTACGCCCTCTGGCAGCGTGACCTGCTGGGCTCCGACAGCGACCCGGGCGAGCCTGATCT ACGCCGCGCGGCGGGGGGCAGGCGCCCGAGTCGGAGACCCTGCCCGTCCAGTACGCCG CCCGGCAGATCGCCCACTGGCGCGAGCGGCTCGACGGCGTGCCGGAGGAGCTGGACCTGC GCGGCTCTTACCGTTTCGAGCGCTTCGCCGACTACCTGGACGCGTTGCGGGCCCACGCCGG TCAGCCTGGCGCCTGGCGCACGCCAACCCGGCCCCCCCTGGACCTGCTGGACGAAG ACCACATCGCGGCCGACGGCTGGTCGATGCGGCCGCTGGCCGGCGACCTGGCGACCGCCT GCGACATGACGCCCAAGATCTCGCAGGGCGTCACCACGGTGGTCACGGGCAATTGCGGCA 328 CGCTGCGTGCTGCTCGCCCCCCGGCGACGCACCCACGTGCTCGTGCTGCTGCTGC CGCCCGGCTTCATCGACTCGCACACCCACGACGACAACTACCTGCTCAG-----GCGTC GGGTCGAGGAGGCGGTCGCCGAAGCGGCCGCGTACGCCTTCGACCTGGCCCGGGAGATCC TCGGCGATCTGTCGGACGCCGCCGCACACCCCGGGTCGACGTGTCGGGCCTGGTGGTCG GCAGCAACACCCCGGGGGGGGGGCGCGACCTGGGCGTGCGCGACCGCATCGCCGCA 154 TGGCCCGGCACGAGGTGCTGCGCACGGTGTTCACGGTCGCCGACGGCGAGCCGTGGCAAC 46289 TGTCCCAATCCGATTCCCAGCCCTTCGACCTGCTGCTCGCGGGGGGCACCCTCATCGACG 605; Similarity Conservative 4.98; 0 Score 86; Pred. No. Mismatches 775; 2e-05 멂 where the polypeptide chemically 24; Length 88421; Indels 24; Gaps 568 46829 628 508 46649 46589 214 448 388 46529 268 94 46469 46409 46349 ω

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iuct= "Evro"
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duct= "EvrL"
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                                                                                                          05-JUN-2000
                                                                                                                                                                                                                                    1287 G
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                               chronic
                                                                                                                                 AAZ87286
                                                                                                                                                      AAZ87286 standard;
              hypercholesterolaemia; crop protection agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             879
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                                                                                                                                                                                                               95698
                           obstructive
                                                                                                         (first entry)
                                                                                                                                                    DNA;
                           pulmonary disease;
                                                                                                                                                      1248
                         respiratory
               g
                                                                                SEQ ID
                                                                                NO:7.
                                                       pikromycin;
                                  asthma;
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Streptomyces venezuelae ATCC15439

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212

TCGCGCCCGGCTTCATCGACTCGCACACCCACGACGACAACTACCTGCTCAGGCGTCGCG TCACCCCGGTCTTCGCCGACATCGACCCGGGACACCGGCAACCTCGACCCGGACCAGGTGG CCATCGGCGATCTGTCGGACGCCGCGCGCGCACACCCCGGGTCGACGTGTCGGGCCTGGTGG

394

211

271

334 151 274

335

152 275 215

439;

Conservative

0

Score 81.8; DB 21; Pred. No. 0.00015; 0; Mismatches 542;

12;

Gaps

other; Length Indels

Similarity

44.28;

92

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biomedical applications, to engineer pHA monomer synthases or to prepare biologically active agents, such as chemotherapeutics, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., bacteria, including as viral parasitic pathogens, or as crop protection agents (e.g., sequences AZ87286-287294 represent desosamine biosynthetic renes from Streptomycas varances.
       Sequence 1248 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     production of biologically active macrolides. The macrolide biosynthetic proteins are useful for synthesis of methymycin, pikromycin, neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or recombinant host cells are useful as biopolymers, e.g., in packaging or recombinant host cells are useful as biopolymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pikromycin, neomethymycin, narbomycin or a combination of these compounds. Recombinant or augmented cells comprising the desosamine and/or macrolide biosynthetic gene clusters are useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryC gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycinity macrolide and the synthesise methymycinity macrolide.
                                                                         . 81777±181-477189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated and purified nucleic acid segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Desosamine and macrolide synthesis of methymycin a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3;
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   177 A;
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                                                                                              94 represent desosamine biosynthetic ATCC 15439, which encode proteins
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   546 C;
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G; 148. T; 0
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                                                  GIYCOSYlated polyketide; modified recombinant bacterial host cell; mRBHC; macrolide; anthracycline; angucycline; avermectin; milbemycin; tetracycline; polyene; polyether: ansamurin.
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          Streptomyces venezuelae
                                                                                                                                                                                            AAD39044 standard; DNA; 1248
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                                ide; anthracycline; angucycline; avermectin;
polyene; polyether; angamycin; isochromanequesi; 4-dehydrase; enzyme; gene; ds.
                                                                                                         venezuelae DesI gene
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                                                                                                                                                                                                                                                                                                                                                               Matches 439;
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           The invention provides a method to alter the sugar structure diversity for a particular metabolite via the recruitment and collaborative action of sugar genes from a variety of sugar biosynthetic pathways to yield a polyketide. The invention also relates to a modified recombinant patterial host cell (mrbic) in which the expression and activity of nucleic acids encoding sugar biosynthetic enzymes has been altered. The mrbics may be cultured to produce the modified sugar products, e.g. a macrolide, anthracycline, ansurgyline, avermectin, milbemycin, tetracycline, polyene, polyether, ansamycin or isochromanequinone. The present sequence is Streptomyces venezuelae sugar (desosamine) biosynthetic gene cluster Desi (4-dehydrase) gene.
                                                                                                                                                                                                                                                                                                                                                            Sequence 1248 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified recombinant bacterial host cells in which the expression activity of nucleic acids encoding sugar biosynthetic enzymes has altered, useful for producing metabolites with altered sugar struc
       332
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                         GCGCCGCCGACCAGCTGCGGAAGGTCGCCGACGAGCACGGCCTGCGGCTGTACTTCGACG
                                                                                                                                    TCACCCCGGTCTTCGCCGACATCGACCCGGACACCCGGCAACCTCGACCCGGACCAGGTGG
                                                                              CCGCCGCGTCACACCCCGCACCTCGGCCGTCGTCGGCGTCCACCTCTGGGGCCGCCCCT
                                                    ACATGACGCCCAAGATCTCGCAGGGCGTCACCACGGTGGTCACGGGCAATTGCGGCATCA
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ZHAO L.
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/transl_except= (pos:1..3, aa:Met)
/note= "CDS does not include start codon"
/partial
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Pred. No. 0.00015;
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                                                                                                                                    neometnymycin; narbomycin; polyhydroxyalkanoate monomer synthase biopolymer; antibiotic; chemotherapeutic; immunosuppressant; astichronic obstructive pulmonary disease; respiratory inflammation;
  26-JUN-1998;
                         25-JUN-1999;
                                                                          W0200000620-A2
                                                                                                  Streptomyces venezuelae ATCC15439
                                                                                                                            hypercholesterolaemia;
                                                                                                                                                                    Desosamine biosynthesis; macrolide; polyketide; methymycin;
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9808-0105537
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                                                                                                                                 inflammation;
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GCTCTTACCGTTTCGAGCGCTTCGCCGACTACCTGGACGCGTTGCGGGGCCACGCCGGCGG

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CCGCGCACGCCTCGGCTGCGCGGTCGACGGCCGGCCGCCGGCAGCCTCGGCGACGCCG

GCCTGGCGCCGCGCACGCCAACCCGCCCGCCCCTGGACCTGCTGGACGAAGGCG GCGCCGCCGACCAGCTGCGGAAGGTCGCCGACGAGCACGGCCTGCGGCCTGTACTTCGACG

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11862 TCACCCCGGTCTTCGCCGACATCGACCCGGACACCGGCAACCTCGACCCGGACCAGGTGG

CCATCGGCGATCTGTCGGACGCCGCGCGCACACCCCGGGTCGACGTGTCGGGCCTGGTGG 211

CCGCCGCGTCACACCCCGCACCTCGGCCGTCGTCGGCGTCCACCTCTGGGGCCGCCCCT TCGCGCCCGGCTTCATCGACTCGCACACCCACGACGACAACTACCTGCTCAGGCGTCGCG 271

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11803

ACATGACGCCCAAGATCTCGCAGGGCGTCACCACGGTGGTCACGGGCAATTGCGGCATCA

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11982

CCACCTGCAACGCCACGGCCGGGCTCCAGCTCCTCGCGCACGCCGGCCTCACCGGCG 11923

Best Loc Matches

Query Match
Best Local Similarity

Conservative

0,

Score 81.8; DB 21 Pred. No. 0.00011; 0; Mismatches 542

DB 21;

Indels Length 12441;

Gaps

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44.28;

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CC The invention relates to an isolated and purified nucleic acid segment CC comprising a desosamine biosynthetic gene cluster, a fragment or its delived from the eryC gene cluster of Saccharopolyspora erythreae or CC delived from the eryC gene cluster of Saccharopolyspora erythreae or CC biosynthetic gene cluster cancides proteins which synthesise methymycin, neomethymycin, narbomycin or a combination of these CC pikromycin, neomethymycin, narbomycin or a combination of these CC compounds. Recombinant or augmented cells comprising the desosamine CC and/or macrolide biosynthetic gene clusters are useful for the production are useful for synthesis of methymycin, pikromycin, neomethymycin and cC are useful for synthesis of methymycin, pikromycin, neomethymycin and CC arbonycin. The alternative termination of polyketide synthesis may be compounded. The compounds produced by the recombinant host cells are useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) CC monomers. The compounds produced by the recombinant host cells are useful constructive pulmonary disease as well as other diseases involving cc antibiotics which are active against a variety of organisms, e.g., cc antibiotics which are active against a variety of organisms, e.g., cc antibiotics which are active against a variety of organisms, e.g., cc bacteria, including multi-drug resistant pneumococci and other
  Sequence 12441 BP; 1704 A; 4294 C; 4686 G;
                                                             bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of polyketides in plants. The present sequence represents the desosamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desosamine and macrolide biosynthetic synthesis of methymycin and pikromycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sherman DH,
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                                               cluster from Streptomyces
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1757 T; 0 other;
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                                                                                                                                                                                                neomethymycin; narbomycin; polyhydroxyalkanoate monomer syntibiopolymer; antibiotic; chemotherapeutic; immunosuppressant; chronic obstructive pulmonary disease; respiratory inflammat;
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                                                                                                                                                                                     hypercholesterolaemia;
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                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                              venezuelae ATCC15439.
                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                                                      desosamine biosynthetic gene cluster pikB
/product= '6834'..7402
                                                                                                                                        Location/Qualifiers
                                            product- "PikB
                                                                            roduct "PikB gene cluster protein #1 ote" "No initiation codon given in the
                                                                                                       artia
                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                     ..2014
                                                                                                                                                                                                                                                                                  entry)
                                 ..6741
                                                                                                                                                                                     crop
                                                                                                                                                                                                                                                                                                                                  13613
       "PikB gene cluster protein
                                                                                                                                                                                     protection
                                                                                                                                                                                                                                                                                                                                  ВP
                                           gene
                                           cluster
                                                                                                                                                                                               respiratory
                                           protein
                                                                                                                                                                                                                               methymycin;
                                                                                                                                                                                               inflammation;
       #3 (AAY77205)"
                                           #2
                                                                            (AAY77204)"
e specification"
                                                                                                                                                                                                                     synthase
                                           "(86608AW)
                                                                                                                                                                                                                               pikromycin;
                                                                                                                                                                                                         asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              982
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The invention relates to an isolated and purified nucleic acid segment comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not carly defrom the eryC gene cluster of Saccharopolyspora erythraea or compounds antibioticus. The invention also relates to a macrolide biosynthetic gene cluster concodes proteins which synthesise methymycin, compounds. Recombinant or augmented cells comprising the desosamine compounds. Recombinant or augmented cells comprising the desosamine compounds. Recombinant or augmented cells comprising the desosamine compounds. Recombinant or augmented cells comprising the desosamine compounds. Recombinant or augmented cells comprising the desosamine compounds. Recombinant or augmented cells comprising the desosamine compounds. Recombinant or augmented cells comprising the desosamine compounds. Recombinant or augmented cells comprising the desosamine compounds protection of polyketide synthesis may be compounded to the alternative termination of polyketide synthesis may be cuseful to prepare novel antiblotics and polyhydroxyalkanoate (PHA) componers. The compounds produced by the recombinant host cells are useful compounder synthases or to prepare biologically active agents, such as chemotheramentics. Immunosuporeasants, agents to treat asthma.
respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-thrus accidents.
                                                                    such as chemotherapeutics, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Figure 32; 438pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desosamine and macrolide biosynthetic synthesis of methymycin and pikromycir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sherman DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         methymycin and pikromycin
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complement (11271...12149)
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complement (12342..13799)
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/transl_except= (pos:8273..8275, aa:Thr)
/transl_except= (pos:8276..8278, aa:Gly)
omplement (10126..11139)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product- "P1kB
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omplement (13706..15043)
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2..8205)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #11 (AAY77212)"
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Best Local
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                                                                                                                                                                                                                                                 12012 ACGGCCTCAACAACCACCAGTACGTGATCGTCGAGATCGACGAGGCCACCACCGGCATCC
                                 11832 CCGAACGCCTCGCCGCGCGCGTGCTGTCCCTGCCGACCGGCACCGCCATCGGCGACGACG
                                                                                                                                                                           11952 ACCGCGACCTCGTCATGGAGGTCCTGAAGGCCGAAGGCGTGCACACCCGGCGCCTACTTCT
                                                                                                                                                                                                                                                                                                                      12072 CCGCCTACCGCGAGCACCTCGCGGACCTCCCCGGCGTCCTCGTCGCCGACCACGACCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12669 CCACCTGCAACGCCACGGCCCCGGCTCCAGCTCCTCGCGCACGCCGCCGGCCTCACCGGCG 12610
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                                                                                                                                                                                                                                                                                                                                                                                                            12132
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                                                                    863 AGGACGTCTCGCTGGACGCGTATCCCTACGTGGCCGGCTCCACCATGCTCAAGCAGGACC 922
                                                                                                                               812 TCGGCCGCTCGCGAGACGCTGCCGCTGATCGAG------GCCGCCATGGCGCGCCC
                                                                                                                                                                                                     752 GCCGCGAGCTGGACGTGCCGGTGGTGATCTCGCACCAAGGTCATGGGCCAGCCCAATT
                                                                                                                                                                                                                                                                                                     692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12549 TCACCCCGGTCTTCGCCGACATCGACCCGGACACCGGCAACCTCGACCCGGACCAGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          632
923 GCGTGCTGCTGGCCGGACGCACCATCATCACCTGGTGCAAGCCCTTCCCCGAACTGAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                              572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               512 TECAGCGCGCCGCCACGACGACGAATCGCGGCCATGCGGGACCTGGCCGAGGAAGCCA 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13613 BP; 1858 A; 4733 C; 5092 G; 1930 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of polyketides in plants. The present sequence represents the desosamine blosynthetic gene cluster (pik) from Streptomyces venezuelae ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 TCGCGCCCGGCTTCATCGACTCGCACGACGACGACGACGACTACCTGCTCAGGCGTCGCG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15439, as given in figure 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                       CGCCGGGCTGCCACGAGCTGGAGCCGTACCGCGGGCAGCCGCACGCCCCGCTGCCGCACA 11833
                                                                                                                                                                                                                                                                                   CCACCGAAGAGATCATCGAGGTGTGCCGGCCGCTGAGCGCGCATGGCGGCATCTACGCCA 691
                                                                                                                                                                                                                                                                                                                                                                                        TGGCCTCACCTCCCTCGACGCGTTTCCCGAGGTCATCGACCGGAACCGGCGCAACCACG 12073
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCCCGGCGGCAGCCCCGCCGGCGGGACCAACGCCAAGATGAGCGAGGCCGCCGCCCA 12133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGCCGCGGTCACACCCCGCACCTCGGCCGTCGTCGGCGTCCACCTCTGGGGGCCGCCCT 12430
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- 밁 Ş CGCGCCACCGCGACACGGCCCCCGCCCCGCTCG 11680 GCCGCGACCTGGATGAAGTCGCGGCCGAGCGCG 1015
- Search completed: May 11, Job time: 1433 secs 2003, 01:57:18

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DB=SPTREMBL_21 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cd1 -LIST=45
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    No. 1s the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
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MEDITINE-21681879; pubMed-11823852;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
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"Acture 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8XQN5
                                                                                                                                EMBL; ALG46083; CAD18338.1; --
Hydrolase; Plasmid; Complete p
SEQUENCE 494 AA; 53186 Mar.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Probable N-acyl-D-glutamate deacylase protein (EC 3
NDED OR RSP1187 OR RS03131.
Raistonia solanacearum (Pseudomonas solanacearum).
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ
EMBL; AJ248283; CAB49065 1; -
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Pfam; PF01979; Adenine_deam; 1.
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Archaea; Euryarchaeota; Thermococci; Thermococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1534 CGCCCCCCCCCAACCCTG 1551
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118 GCCGACCTGGGCGTGCGCCGACCGCATCGCCGCCATCGGCGATCTGTCGGACGCCGCC
                                                                      58 TTCGACCTGCTGCTGCGGGGGGGGCACCCTCATCGACGGCAGCAACACCCCGGGGCGGCGGCGC
                                           4 TyraspileValileLysAsnGlyLysIleValAspGlyThrGlyAsnProTrpPheArg
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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-CAGCCGGCCGCCCATCTACTTCATGATGGACGAACCCGACGTG
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US-10-009-782-1 (1-1758) x Q93JK8
                                             Query Match:
                                                                               Percent Similarity
                                                                                                                             Alignment
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                                                                  Local
                                                                                                                                                                                                                                                      Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quall M.A., Kideser H., Harris D.E., Chandra G., Chen C.W., Collins Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth Huang C.-H., Kideser T., Larke L., Murphy L., Oliver K., O'Neil S. Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.
                                                                                                                                                                         coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL591857; CAC40599.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1902;
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AlaLeu-AlaGluTyrValGlyArgThrValLeuGluSerAlaArgLeuArgGlyGluSe
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                                                                                         GlySerHisGlyValProMetGluTrpGluThrIleGluIleSerGlyThrGlyAspPro
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Ol-JUN-2001 (TIEMBLIEL. 17, Last sequence update)
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Hypothetical protein CC3460.
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MEDLINE-21173698; PubMed-11259647;
Nierman W.C., Feldblyum T.V., Laub
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Oy 58 TTCGACCTGCTGCGCGGCCACCCCCACCGCCACCACACACCCCGGGGGCGGGGCGGGCGCGCCCCCC
TYCASCITGCTGGGGGGGGCACCCCTCATCGACGGCAGCACACCCCGGC ::: :::

Qy 938 CTGCTGGCCGACCGACCACCATCACCATCACCTGGCTCCCCGAAACTGAACCGGGCCCCGGCGCGCACCTGAACCGGACCGACC		•		
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Moghaddam A., Annis I
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Submitted (MAR-1997) to
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J. Virol. 74:5921-5932(2000).
SEQUENCE FROM N.A.
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Rivailler P., Quink C., Wang F.;
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                                                ThrArgGlnArgProGlyH1sProProProGluArgGlySerGlyProArgGlyThrArg
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	232	GlyProGluProArgThrAr	213	В
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	593	GGAAATCGCGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCATCGGCAT	534	Qy
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	533	GGGCCATTCAACGCTGCGCGCGCGGTCATGCCGGACTTGCAGCGCGCCGCCGACGACGA	474	QY
	182	AlaAlaAspProAlaAspProValGlyHis-ProAlaAlaProArgAla-ProGlyProG	163	B
	473	CGCCGACTACCTGGACGCGTTGCGGGGCCACGCCGGCGGCGGCCGTCAACGCCGGCTGTATGGT	414	δ
·	162	ArgAlaProGlyProGluProArgThrArgLeuGlnProAlaThrProArgArgSerGly	143	D.
	413	CCTGGACCTGCTGGACGAAGGCGGCTCTTACCGTTTCGAGCGCTT	369	δ.
	142	ThrProArgArgSerGlyAlaAlaAspProAlaAspProValGlyHisProAlaAlaPro	123	8
•	368	GCCGCTGGCGCACGCCAACCCGCCCCCC	339	Q
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1300		Qy 1		
2689	2669 OAlaAlaAlaAlaAlaAlaThrAlaAlaValPrOAlaPrOGlyValGlyPrOGlyGl	Db 2	,	
1240		Qy 1		
2669	2650 uProArgProProGlnAlaGlnAlaGlnAlaProAlaThrAlaProThrGlyProPr	Db . 2		
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Qy 1495 GCCGGGCTCAGGCGGCGTGCGTGCGAGCACGCCGGCATGCTGGCCGGTGAACGCCT 1436 ::: 110 AlaGlyGlnArgProSerGlyProThrGlyGlyHisProAlaAlaProGlyAlaPro 128 Qy 1435 GCTCTTGCCAGACCGGCGCGCTTGACGTACACGGAATGGATGCCGGCGGGCG	Oy 1597 GGGCCGTATTGCGAGCGGAGGGAGGGGGGGGGGGGGGGG	a · o a o	RESULT 11 Q9Q5K9 ID Q9Q5K9 ID C9Q5K9; AC Q9Q5K9; DT 01-MAY-2000 (TTEMBLTel. 13, Created) DT 01-MAY-2000 (TTEMBLTel. 13, Last sequence update) DT 01-MAY-2000 (TTEMBLTel. 13, Last annotation update) DT 01-MAY-2000 (TTEMBLTel. 13, Last annotation update) DT VITUSES; daDNA viruses, no RNA stage; Herpesviridae; OC VITUSES; daDNA viruses, no RNA stage; Herpesviridae; OC VITUSES; daDNA viruses, no RNA stage; Herpesviridae; OC VITUSES; daDNA viruses, no RNA stage; Herpesviridae; OC VITUSES; daDNA viruses, no RNA stage; Herpesviridae; OC VITUSES; daDNA viruses, no RNA stage; Herpesviridae; OC VITUSES; daDNA viruses, no RNA stage; Herpesviridae; OC VITUSES; daDNA viruses, no RNA stage; Herpesviridae; OC VITUSES; daDNA viruses, no RNA stage; Herpesviridae; OC SEQUENCE FROM VITUSES, no RNA stage; Herpesviridae; OC STRAIN-BABOON LYMPHOCRYPTOVIRUS BA65; RN SEQUENCE FROM N.A. RA Hayward G.S.; Ling P.D., Loeb D.D., Pagano J.S., Hayward S.D., RA Hayward G.S.; Ling P.D., Loeb D.D., Pagano J.S., Hayward S.D., RA Hayward G.S.; STRAIN-BABOON LYMPHOCRYPTOVIRUS BA65; RN SUBMITTED (1999) to the EMBL/GenBank/DDBJ databases. SQUENCE 608 AA; 60458 MW; 4BF82ACB0A029627 CRC64;	Db 2857 rProProProSerAspProProProValGlnPh 2867 Qy 1654 GCCGGAAAATGACCCTGCAAGACCTGTCGCAGGCCAGCGGCATCGCGGGTCTCGACCCTG 1713
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MEDLINE=20440633; PubMed=10970361;
Rao P., Jiang H., Wang F.;
"Cloning of the rhesus lymphocryptovirus viral capsid antigen
Epstein-Barr virus-encoded small RNA homologues and use in dia
of acute and persistent infections.";
                                                                                                                                                                                                           "Structural, functional, and nuclear antigen 3A, 3B, and 3 lymphocryptovirus.";
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                                                                                                                                          SEQUENCE FROM N.A. STRAIN-LCL8664;
                                                                                                                                                                                                                                                                                                                                        MEDLINE=20304984; PubMed=10846073;
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Submitted (JUN-2001) to the
EMBL; AY037858; AAK95470.1;
SEQUENCE 890 AA; 95097 M
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One P., Quink
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	GGCCGGGTCGAACACCACCA 1322		y 1369 b 199
	-CGTTGACGTACACGGAATGGATGCCGGCGCGCGCGCTCGGTAGGGT 1370 :::	GlyThrArgProPr	y 1414 b 181
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STRAIN-186;
STRAIN-186;
Huang C.M., Asmundson R.V., Yu P.L.;
"Nucleotide sequence of a cellulase gene complex from Ruminococcus
flavefaciens strain 186 coding for multi-cellulase activities.";
Submitted (SEP-1990) to the EMBL/GenBank/DDBJ databases.
EMBL; X56082; CAA39559.1; -.
EMBL; X56082; CAA39559.1; -.
STOTIENCE 680 AA; 75503 MW; 5A589F334846DD6F CRC64;
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Q52747;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Lachnospiraceae; Ruminococcus.
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Search completed: May 11, 2003, 12:15:53
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                           AATTTCGGCCGCTCGCGCGAGACGCTGCCGCTGATCGAGGCCGCCATGGCGCGCCAGGAC
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                                                                                                                 CAGGACCCGCTCTGGGCCCTGCCGCACGCGGTGAGCCCCTTGGCCATGAGCCGCCGCTAC
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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
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APPLICANT: Liu, H.
APPLICANT: Loo, I.
APPLICANT: APOLICANT: ANO. I.
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
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TYPE: DNA
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Patent No. 6265202
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335 TCACCCCGGTCTTCGCCGACATCGACCCGGGACACCGGCAACCTCGACCCGGACCAGGTGG
                         152 CCATCGGCGATCTGTCGGACGCCGCCGCGCACACCCGGGTCGACGTGTCGGGCCTGGTGG 211
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                                                                                                                                         868 GTCTCGCTGGACGCGTATCCCTACG---TGGCCGGCTCCACCATGCTCAAGCAGGACCGC
                                                                                 CCACCTGCAACGCCACGGCCGGGCTCCAGCTCCTCGCGCACGCCGGCCTCACCGGCG
                                                      GAGCCCGCCCCGCCTGCCCCCGCTCTGGCCCGAGCAGCCCGGCCTCGTCGTCCCAGCG
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Sequence 3, Application US/09105537A
Patent NO. 6265202
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Sherman, D.H.
APPLICANT: STACO, L.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
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; LENGTH: 13613
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-3
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Best Local Similarity
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ACATCCGCCGGGTCGCCGACCTGCTGCGCGTCTCTGCGCGACCGGCGAACTGACCG
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                             GCGTGCTGCTGGCCGGACGCACCATCATCACCTGGTGCAAGCCCCTTCCCCGAACTGAGCG 982
                                                             CCGAACGCCTCGCCGCGCGCGTGCTGTCCCTGCCGACCGGCACCGCCATCGGCGACGACG
                                                                                           AGGACGTCTCGCTGGACGCGTATCCCTACGTGGCCGGCTCCACCATGCTCAAGCAGGACC 922
                                                                                                                             CGCCGGGCTGCCACGAGCTGGAGCCGTACCGCGGGCAGCCGCACGCCCCGCTGCCGCACA 11833
                                                                                                                                                   TCGGCCGCTCGCCGCAAGACGCTGCCGCCTGATCGAG------GCCGCCATGGCGCGCCC
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Pred. No. 2.1e-07;
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GENERAL INFORMATION:
APPLICANT: Stanford University
APPLICANT: Stanford University
APPLICANT: Khosla, Chaitan
TITLE OF INVENTION: NON-STEROIDAL ESTROGEN-RECEPTOR
FILE REFERENCE: 28600-20210.00
CURRENT APPLICATION NUMBER: US/09/773,816
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/243,458
PRIOR FILING DATE: 2000-10-25
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1
SOPTWARE: FASTSEQ for Windows Version 4.0
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; LOCATION: (1)...(23623)
; OTHER INFORMATION: n = .
US-09-773-816-1
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Best Local Similarity
Matches 667; Conserv
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LENGTH: 23673
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                                 GCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCATCGGCATTTCGACCGGC
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ilarity 42.4%; Pred. No. 1.5e-06;
Conservative 0; Mismatches. 891;
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                                                   GACCGCTGGGCCCGCTTCCGCCGCTATGGCGCGGAACGCACCACCGACGCCGAGATCACC 7189
                                                                                AACCGCTACATGGCCCCTCCCCTCCGCTCGCAATACGGCCCCACCCGATATCGTGGGCAAG 1617
                                                                                                            GACGCGATCGCGGCCTCGCGGAGTTGTCCCCCCTCGACGGCCACCAGTTGGTCGCC
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Best Local Similarity 44.7%;
Matches 334; Conservative
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LENGTH: 5970
TYPE: DNA
ORGANISM: Streptomyces venezuelae
-09-320-878-21
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                                                                                                                                       421 AGGTCTTCAGCTTC---CACGCCACCAAGGCCGTCAACGCCTTCGAGGGCGGCGCGCCGTCG
                                                                                                                                                                              392 GCTCTTACCGTTTCGAGCGCTTCGCCGACTACCTGGACGCGTTGCGGGGCCACGCCGGCGG
                                                                                                                                                                                                                       332 GCCTGGCGCCGCTGGCGCACGCCAACCCGGCCCCCCCTGGACCTGCTGGACGAAGGCG 391
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512 TGCAGCGCCGCCGACGACGAGGAAATCGCGGCCATGCGGGACCTGGCCGAGGAAGCCA 571
                                                       LICANT: ASHLEY, Gary
LICANT: BETLACH, Melanic
LICANT: BETLACH, Mary C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LICANT: McDANIEL, Robert LICANT: TANG, Li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn
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LING DATE: 1999-02-08
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
                                                               EATURE:
                                                                                                                                                                                                                              OLECULE TYPE:
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                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: Februa CLASSIFICATION: 435
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                                                                                                                              LOCATION:
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Sutton, Kimberly L
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Best Local Similarity 42.5
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ATGAAGTCGCGGCCGAGCGCGAAATCCAAGTACGACGTGGTGCCCGAGCTGCAGCCGG
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                                             CCGGAGCGCTGCCCCCCTGCCCCTCACCGCCTACGGCATACGCGACGCCCCGCACC----
                                                                                                       TGCAGGCCGGTCCCGACACCGTCGGGGAGATGCTCGGGGGAACTGCTGGAACTGTTCGCGG
                                                                                                                                                                                             GCCGCTCGCGCGAGACGCTGCCGCTGATCGAGGCCGCCATGGCGCGCCAGGACGTCTCGC
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Pred. No. 3
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; Patent No. 5858773
; GENERAL INFORMATION:
APPLICANT: MARCODIER,
APPLICANT: GUGLIEMI,
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                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                       APPLICANT: MAZODIER, Philippe
APPLICANT: GUGLIEMI, GETARG
TITLE OF INVENTION: REGULATORY NUCLECTIDE SEQUENCE OF
TITLE OF INVENTION: INITIATION OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1652
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                       STREET: George Mason Bldg.,
CITY: Alexandria
STATE: Virginia
                                                                                       COUNTRY: United States ZIP: 22313-1404
                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                    Burns, Doane, Swecker & Mathis
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Version
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; LOCATION:
US-08-461-775-8
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Best Local Similarity 46.9%;
Matches 234; Conservative
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   570
                                                         510 CGGTGTCATCACCGTCGAGGAGTCCAACACCTTCGGTGTCGACCTGGACTTCACCGAGGG
                                                                                                      717
                                                                                                                                        450
                                                                                                                                                                                              330 CTCCCCGGCCGCCTGAAGAAGGCCATCGACGCCGCCGTCGCCGCCGTCTCCGCCGAGCT 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,:
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: FR 9011186
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ATTORNEY/AGENT INFORMATION:
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-APPLICATION NUMBER: US/08/461,775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                GATCTCGCACCACAAGGTC 795
                                                                                         CGCGCAGGACAAGCAGGTCGGCGAGCTCATCGCCGAGGCGATGGACAAGGTCGGCAAGGA
                                                                                                                                                          CCGGCCGCTGAGCGCGCATGGCGGCATCTACGCCACCACATGCGCGACGAAGGCGAGCA 716
CATGGCCTTCGACAAGGGC 588
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Pred. No. 3.2e-06;
0; Mismatches 265
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RESULT 8 US-09-031-606-8

Sequence 8, Application US/09031606 Patent No. 6153404

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; LOCATION:
US-09-031-606-8
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Best Local Similarity
Matches 234; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                  537 AATCGCGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCCATCGGCATTTC
                                                                                                                                                                                             477 CCATTCAACGCTGCGCGCCGCGCTCATGCCGGACTTGCAGCGCGCCGCCGCCACCGACGAGGA 536
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REFERENCE/DOCKET NUMBER: 011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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APPLICATION NUMBER: FR 9
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CLASSIFICATION:
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GCTCGACACCGCGCGCGCGATCGACGACAAGTCCGACATCGCCGCCGCTCGCCGCTCTC
                                       GACCGGCGCCTTCTACCCGCCCCGCCCCCCCCCCCCACCACCGAAGAGATCATCGAGGTGTG
                                                                          CTCCCCGGCCGCCTGAAGAAGGGCATCGACGCCGCCGTCGCCGCCGTCTCCCGCCGAGCT 389
                                                                                                                                                         CGCGACCGTGCTGGCCAGGCGCTGGTCCGCGAGGGCCTGCGCAACGTCGCCGCCGGCGC
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EDNESS: double
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WENTION: REGULATORY
WENTION: INITIATION
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Pred. No. 3.2e-06;
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US-08-461-775-10
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Patent No. 58
                                                                                                                                                                                                                                                                             TELEFAX: (703) 836-20
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,313
FILING DATE: 10-MAY-1993
                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
         357
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                                                                                      Local Simbes 234;
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                                    90
                                                                                                                                                         NAME/KEY:
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CCCGCCCGCCCCTGGACCTGCTGGACGAAGGCGCTCTTACCGTTTCGAGCGCTTCGC 416
                          GGCCCCAAGGGCCGCAACGTCGTCATCGACAAGAAGTTCGGCGCCCCGACCATCACCAA 149
                                                     ASSIFICATION: 435
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                                                                                    Score 75; DB 2;
Pred. No. 3.3e-06;
0; Mismatches 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington
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US-09-031-606-10
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 10-MAY-1
                                           REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                       FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                         APPLICATION NUMBER: FR 90 FILING DATE: 10-SEP-1990
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                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                   RY: United 22313-1404
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                                                                                                           Crane-Feury, Sharon E
                                                                                                                                                                                                                                                                                                                                                                                                    Virginia
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                                 (703)
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                             836-2021
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RESULT 11
US-08-458-568A-11/c
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Best Local Similarity
Matches 234; Conserv
                                                                                                                                                                                                                                                                                                                                        quence 11, Application US/08458568A tent No. 5821339
                                                                                                                                                                                                                                                                                                                    ENERAL INFORMATION:
                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (ger
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                                                                                                                                                                                                                                                                                   PPLICANT:
           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                           COUNTRY: U
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                                                                                                                                                                                                     RRESPONDENCE ADDRESS
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                                                                                                                                                          DDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris
STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                            BER OF SEQUENCES:
                                                                                                                                                                                                                                        LE OF INVENTION: Composition infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGGCCGCTGAGCGCGATGGCGGCATCTACGCCACCCACATGCGCGACGAAGGCGAGCA 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAGCTCGTCAAGGAGGTGGCGACCAAGACCAACGACATCGCGGGTGACGGCACCACCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCGCCCCCCCCTGGACCTGCTGGACGAAGGCGGCTCTTACCGTTTCGAGCGCTTCGC 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGTGTCATCACCGTCGAGGAGTCCAACACCTTCGGTGTCGACCTGGACTTCACCGAGGG 569
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                                                                                                                                                Philadelphia
                                                                                                                             PA
                                                                                                               USA
                                                                                                                                                                                                                                                                                                   Schaffer, Priscilla A.
WordPerfect 5.1
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                                                                                                                                                                                                                                                    Compositions and Methods for Treatment of Herpesvirus
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Pred. No. 3.3e-06;
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Best Local
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                                   4645 CGCCGCGCCCAGGCCGGCCGCGTGGCCGTCGAGTGCCTGGCCGCCGCGCGATCCTG
                                                                                                                                                                                              4705
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                             4825 AGATGACGAGGGGGTCGCCGCCGTCGCCGCCGCCGCACCGGGCGAGCGCGCGGTGCCCGC 4766
                                                                                                                                                                                                                                                                                                                                                                                                              4885 CCTGTTGGCGCGCGAGAACGCGGCGCTGACGGGGGCCGCGGGGAGCCCCGGCGCGCGGCGC 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              429
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                                                                                                                                               664 CTGAGCGCGCATGGCGGCATCTACGCCACCCACATGCGCGACGAAGGCGAGCACATCGTG 723
                                                                                                                                                                                                                                                                                                  549 GCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCC----ATCGGCATTTCGACCGGC 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 CCTGGACCTGCTGGACGAAGGCGGCTCTTACCGTTTCGAGCGCTTCGCCGACTACCTGGA 428
784 CACCACAAGGTCATGGGCCAGCCCAATTTCGGCCGCTCGCGCGAGACGCTGCCGCTGATC 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 GGTCGACGTGTCGGGGCTGGTCGCGCCCCGGCTTCATCGACTCGCACACCCCACGACGA 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 CAACTACCTGCTCAGGCGTCGCGACATGACGCCCAAGATCTCGCAGGGCGTCACCACGGT 308
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PRIOR APPLICATION DATA:
US 08/065,146
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nes 581; Conserv
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STRAIN: Herpes Simplex virus Type 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                      GCCGCGCTGGAGGAAACCTTCCGCATCGGCCGCGAGCTGGACGTGCCGGTGGTGATCTCG 783
                                                                                                                                                                                    GCGCGCCGCGGTCATGCCGGACTTGCAGCGCGCCGCCGACGACGAGGAAATCGCGGCCAT 548
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Pred. No. 5.2e-06;
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4586

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Gaps

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Sequence 1, Application US/09105537A
Patent No. 6285202
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: ANO, L.
TITLE OF INVENTION: DNA encoding methymycin and FILE REFERENCE: 600.438US1
                                                                                                                                                                                                                                                                           RESULT 12
US-09-105-537-1
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; TYPE: DNA
; ORGANISM: Streptomyces
US-09-105-537-1
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                                                           SEQ ID NO 1
                                                                      NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                  CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
                                             LENGTH: 15872
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Best Local Similarity
Matches 586; Conserv
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                                                                                            GGTCTCGCGACCGCCCATGTCCACGGCGCACCCTTGGACCGGGCGTCGTTCTTCCCGGAC
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                                 GGGCGCCGCACGGACCTGCCCACGTACGCCTTCCGGCGCGAGCACTACTGGCTGACGCCC
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Pred. No. 7e-06;
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 5858
                                                                                                                                                         TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                        TOPOLOGY: 1:
MOLECULE TYPE:
08-461-775-9
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                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,:
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: FR 9011186
FILING DATE: 10-SEP-1990
                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-035
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6050
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                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
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LE OF INVENTION: REGULATORY NUCLEOFIDE SEQUENCE OF THE

LE OF INVENTION: INITIATION OF TRANSCRIPTION
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                                                                                                                                        2167 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     United States
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 46.78;
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 Score 73.4; DB 2; Pred. No. 6.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 10-MAY-1
APPLICATION NUMBER: F
                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MAZODIER, APPLICANT: GUGLIEMI,
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                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                             STREET: George M. CITY: Alexandria STATE: Virginia
                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States 
ZIP: 22313-1404
                                                               FILING DATE:
    REGISTRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATCTCGCACCACAAGGTC
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VATION NUMBER: 36,113
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George Mason Bld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAZODIER, Philippe
                                                               10-SEP-1990
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                                                                            FR 9011186
                                                                                                  us 08/050,313
                                                                                                                                                                                               us/09/031,606
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Sequence 11,
Patent No. 58
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                 COMPUTER READABLE FORM:
                                                                                                                 APPLICANT: GGGLIEMI, GERARD
TITLE OF INVENTION: REGULATORY
TITLE OF INVENTION: INITIATION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESCEF BUSINESS
                                                                                                                                                                                                                NERAL INFORMATION:
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       MEDIUM TYPE:
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                                  COUNTRY: United
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                                                                                                                                                                                                                                                                                                                                                                                              CATCGTGGCCGCGCTGGAGGAAACCTTCCGCATCGGCCGCGAGCTGGACGTGCCCGGTGGT 776
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                                                                         T: George Mason Bldg., Alexandria
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                                                            Virginia
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                                             United States
                                                                                                                                                                              GUGLIEMI,
                                                                                                                                                                                            MAZODIER, Philippe
                                                                                                      Burns, Doane,
Floppy disk
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Pred. No. 6
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                                                                                Washington & Prince Sts
                                                                                                                                            NUCLEOTIDE SEQUENCE OF OF TRANSCRIPTION
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              Search completed: May 11,
Job time : 235 secs
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US-08-461-775-11
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1418 CATGGCCTTCGACAAGGGC 1436
                                                                        1358 CGGTGTCATCAACGTCGAGGAGTCCAACACCTTCGGTGTCGACCTGGACTTCACCGAGGG 1417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2668 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      417 CGACTACCTGGACGCGTTGCGGGCCACGCCGGCGGCGGCCGTCAACGCCGCCTGTATGGTGGG 476
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FILING DATE: 10-SEP-1990
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 CGTCACCACGGTGGTCACGGGCAATTGCGGCATCAGCCTGGCGCCGCTGGCGCACGCCAA 356
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mes 233; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 01
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                                       GATCTCGCACCACAAGGTC 795
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                                                                                                               CATCGTGGCCGCGCTGGAGGAAACCTTCCGCATCGGCCGGGGCGGGAGCTGGACGTGCCGGGTGGT 776
                                                                                                                                                           CGCGCAGGACAAGCAGGTCGGCGAGGCTCATCGCCGAGGCGATGGACAAGGTCGGCAAGGA
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                                                                                                                                                                                              CCGGCCGCTGAGCGCGATGGCGGCATCTACGCCACCACATGCGCGACGAAGGCGAGCA 716
                                                                                                                                                                                                                                          GCTCGACACCGCGCGCCCGATCGACGACAAGTCCGACATCGCCGCCGTCGCCGCGCGCTCTC 129
                                                                                                                                                                                                                                                                                 GACCGGCGCCTTCTACCCGCCGCCGCCGCCGCGCCACCGAAGAGATCATCGAGGTGTG 656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATTCAACGCTGCGCGCGCGCTCATGCCGGACTTGCAGCGCGCCGCCCACCGACGAGGA 536
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836-2021
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EM: PC-DOS/MS-DOS
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Pred. No. 7e-06;
0; Mismatches 266
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Gaps

2003, 10:52:38

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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118
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                                                                                                                                                                                                                                                                                                          Score
81.88
81.88
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seq length: 2000000000
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Match
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1758
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/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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                              12441
13613
13613
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US-09-860-846-7
US-09-986-384B-7
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US-09-986-384B-3
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US-09-986-288A-1
US-09-815-242-4056
US-09-988-384B-30
US-09-988-384B-30
US-09-988-384B-30
US-09-988-384B-30
US-09-988-384B-30
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       Sequence 1, Appli
Sequence 5, Appli
Sequence 1, Appli
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Sequence 1, Appli
Sequence 1, Appli
Sequence 30, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 30, Appl
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Sequence 5
Sequence 5
Sequence 1
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Sequence 1
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Sequence 7, Appli
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			Sequence 4009, Ap	Sequence 1, Appli	Sequence 34, Appl	Sequence 34, Appl	4	Sequence 40, Appl	Sequence 40, Appl	Sequence 40, Appl	Sequence 784, App	Sequence 1, Appli	Sequence 7834, Ap	Sequence 2, Appl1	Sequence 1, Appli	Sequence 7984, Ap	Sequence 4, Appli	Sequence 4052, Ap	Sequence 13, Appl	13,	Sequence 13, Appl	e 32	Sequence 32, Appl	Sequence 32, Appl		Sequence 5, Appl1

ALIGNMENTS

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NAME/KEY misc_feature
LOCATION: (70659)..(71906)
OTHER INFORMATION: ORF 19; positive strandedness
NAME/KEY misc_feature
LOCATION: (73439)..(71964)
OTHER INFORMATION: ORF 20; negative strandedness
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LOCATION: (74216)..(73563)
OTHER INFORMATION: ORF 21; negative strandedness
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LOCATION: (7524)..(74213)
OTHER INFORMATION: ORF 22; negative strandedness
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LOCATION: (39713)..(65800)
OTHER INFORMATION: ORF 14; P
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LOCATION: (39713)..(65800)
OTHER INFORMATION: ORF 15; P
NAME/KEY: misc_feature
LOCATION: (65826)..(66530)
OTHER INFORMATION: ORF 15; P
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LOCATION: (67384)..(70059)
OTHER INFORMATION: ORF 17; p
NAME/KEY: misc_feature
LOCATION: (70099)..(70662)
OTHER INFORMATION: ORF 18; F
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LOCATION: (13617)..(12802)
OTHER INFORMATION: ORF 9; negative strandedness
NAME/KEY: m1sc_feature
LOCATION: (15203)..(13614)
OTHER INFORMATION: ORF 10; negative strandedness
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LOCATION: (66546)..(67370)
DTHER_INFORMATION: ORF 16;
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"HER INFORMATION: ORF 8; negative strandedness
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HANKEYEY: 1875_feature 100ANION: (8773), 168803) COTHER INFORMATION: 08F 33: positive strandedness: N-terminus only 100ANION: (87734), 1880400 100ANION: (87734), 18804000 100ANION: (87734), 188040000 100ANION: (87734), 188040000 100ANION: (87734), 188040000000000000000000000000000000000
COCHET INFORMATION: (08F 32: positive strandedness: NAME/KEY: nisc.feature LOCATION: (0873): (08603) OTHER INFORMATION: (08F 32: positive strandedness: N-terminus only -09-976-059-1 ORDER INFORMATION: (08F 33: positive strandedness: N-terminus only -09-976-059-1 SECT. LOCAL SIMILATIVE 43.1%: SCOTE 86; DB 9; Length 88421; BEST. LOCAL SIMILATIVE 43.1%: Pred. No. 1e-10; SET. LOCAL SIMILATIVE A1.1%: Pred. No. 1e-10; SET. LOCAL SIMILATIVE 43.1%: Pred. No. 1e-10; SET. LOCAL SIMILA
NYEWY, MESS_feature \$TRONN, (08737), (08603) **RINNORMATION: OBF 32; Positive strandedness; N-terminus only \$\$76-059-1 **RINNORMATION: OBF 33; Positive strandedness; N-terminus only \$\$76-059-1 ***Index: Observative of the strandedness of th

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                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 43
SOFTWARE: FRATSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 1248
TYPE: DNA
                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                           APPLICANT: Zhao, L. TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/860,846
CURRENT FILING DATE: 2001-05-18
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                  ORGANISM: Streptomyces venezuelae 09-860-846-7
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                                                              CCACCTGCAACGCCACGGCCGGGCTCCAGCTCCTCGCGCACGCCGCCGCCTCACCGGCG
                                                                                                          CCGAGATCACCGTCGCGGCGCTCGTCGCCGAGCAGTGCGCCCGCACGCCGGGTGCGGTCG
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439; Conserv
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                                                                                                                                              Conservative
                                                                                                                                                         4.78;
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                                                                                                                                          Score 81.8; DB 9;
Pred. No. 1.4e-09;
0; Mismatches 542;
                                                                                                                                                                  Length 1248;
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APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin
FILE REFERENCE: 600.536US1
CURRENT APPLICATION NUMBER: US/09/988,384B
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: PCT/US99/14398
                                                                          APPLICANT:
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RESULT 3
US-09-988-384B-7
                                                     Sequence 7, Application US/09988384B Publication No. US20030073824A1 GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1052 CCGAACGCCTCGCCGCGCGCGTGCTGTCCCTGCCGACCGGCACCGCCATCGGCGACGACG
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; SEQ ID NO 7
; LENGTH: 1248
; TYPE: DNA
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Best Local :
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PRIOR APPLICATION NUMBER: US C
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 53
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Local Similarity 44.2%;
es 439; Conservation
CCGAACGCCTCGCCGCGCGCGTGCTGTCCCTGCCGACCGGCACCGCCATCGGCGACGACG
                           AGGACGTCTCGCTGGACGCGTATCCCTACGTGGCCGGCTCCACCATGCTCAAGCAGGACC 922
                                                                                                                                              GCCGCGAGCTGGACGTGGTGGTGATCTCGCACCACAAGGTCATGGGCCAGCCCAATT
                                                                                                                                                                                   ACGGCCTCAACAACCACCAGTACGTGATCGTCGAGATCGACGAGGCCACCACCGGCATCC
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Pred. No. 1.4e-09;
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APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
APPLICANT: 2hao, L.
TITLE OF INVENTION: DNA encoding methymycin and
FILE REFERENCE: 600.438US1
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US/09/861,289
CURRENT FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FRASTSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 1248
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; ORGANISM: Streptomyces venezuelae
US-09-861-289-7
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Best Local
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APPLICANT: Sherman, D.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09861289
Patent No. US20020110897A1
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                                                                                     CCGTCAACGCCGCCTGTATGGTGGGCCATTCAACGCTGCGCGCCGGGTCATGCCGGACT
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                                                                                                                                                                                                                                                                                               CCGCCGCGGTCACACCCCGCCACCTCGGCCGTCGTCGGCGTCCACCTCTGGGGCCGCCCCT
                      TGCAGCGCGCCACCGACGAAGGAAATCGCGGGCCATGCGGGACCTGGCCGAGGAAGCCA
                                                          TCACCGACGACGCCGACCTCGCCGCCCGGATCCGCGCCCTCCACAACTTCGGCTTCGACC
                                                                                                                    AGGTCTTCAGCTTCCA----CGCCACCAAGGCCGTCAACGCCTTCGAGGGCGGCGCGCGTCG
                                                                                                                                              GCTCTTACCGTTTCGAGCGCTTCGCCGACTACCTGGACGCGTTGCGGGGCCACGCCGGCGG
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Xue, Y.
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Pred. No. 1.4e-09;
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                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                          SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09988384B publication No. US20030073824A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                  -09-988-384B-3
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PRIOR APPLICATION NUMBER: US 09/105,537
PRIOR FILING DATE: 1998-06-26
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin
FILE REFERENCE: 600.536US1
CURRENT APPLICATION NUMBER: US/09/988,384B
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: PCT/US99/14398
                                                                                                                                                                                                                                           LENGTH: 12441
TYPE: DNA
ORGANISM: Streptomyces venezuelae
                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
11862 TCACCCCGGTCTTCGCCGACATCGACCCGGACACCGGCAACCTCGACCCGGACCAGGTGG
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                                                                                                          CGCGCCACCGCGACACGCCCCCCCCCCCCCCCCCCC 1204
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Pred. No. 1.1e-09;
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                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                       Sequence 3, Application US/09860846 Patent No. US20020164742A1
                                            APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/860,846
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537 PRIOR FILING DATE: 1998-06-26 NUMBER OF SEQ ID NOS: 43
                                                                                                                       APPLICANT:
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; TYPE: DNA
; ORGANISM: Streptomyces
US-09-860-846-3
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SEQ ID NO 3
                                                                                                                                                       11952 ACCGCGACCTCGTCATGGAGGTCCTGAAGGCCGAAGGCGTGCACACCCCGCGCCTACTTCT
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                                        CCGAACGCCTCGCCGCGCGCGTGCTGTCCCTGCCGACCGGCACCGCCATCGGCGACGACG 11773
                                                                   AGGACGTCTCGCTGGACGCGTATCCCTACGTGGCCGGCTCCACCATGCTCAAGCAGGACC
                                                                                               TCGGCCGCTCGCGAGACGCTGCCGCTGATCGAG------GCCGCCATGGCGCGCC
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Pred. No. 1.1e-09;
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; ORGANISM: Streptomyces venezuelae
US-09-861-289-3
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Best Local S
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Patent No. US20020110897A1
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TITLE OF INVENTION: DNA encoding methymycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/861,289
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR EPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
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                                                               TGCCCGGCGGCAGCCCCGCCGGCGGGACCAACGCCAAGATGAGCGAGGCCGCCGCCGCCCA 12133
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                                                                                                                                                                  CCGTCAACGCCGCCTGTATGGTGGGCCATTCAACGCTGCGCGCCGCCGGTCATGCCGGACT 511
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439; Conservation
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Pred. No. 1.1e-09;
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; TYPE: DNA
; ORGANISM: Streptomyces refuineus subspecies thermotolerans
US-10-166-087-45
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CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.0
SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 45, Application US/10166087 Publication No. US20030077767A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zazopoulos, Emmanuel TITLE OF INVENTION: Genes and proteins for the biosynthesis of anthramycin FILE REFERENCE: 3014-2US
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APPLICANT: Farnet, Chris
APPLICANT: Staffa, Alfredo
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                                                     CTCGCCTTCGTGCTGCACCGGCACACCGGGCAGGACGACATCCTCCTCGGCGTCCCG
                                                                           GTCGCGCCCGGCTTCATCGACTCGCACACCACGACGACGACGACTACCTGCTCAGGCGTCGC
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Pred. No. 4.6e-09;
0; Mismatches 658;
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RESULT 9 US-10-166-087-1

Sequence 1, Application US/10166087 Publication No. US20030077767A1 GENERAL INFORMATION:

APPLICANT: Ecopia Biosciences Inc. APPLICANT: Farnet, Chris APPLICANT: Staffa, Alfredo APPLICANT: Zazopoulos, Emmanuel

APPLICANT: Farnet, Chris
APPLICANT: Staffa, Aliredo
APPLICANT: Zazopoulos, Emmanuel
TITLE OF INVENTION: Genes and proteins for
FILE REFERENCE: 3014-2US

the blosynthesis of anthramycin

CURRENT APPLICATION NUMBER: US/10/166,087
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 51

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                                  GGCCCGACCATGATCGGCTCCGACGGCCTGCCGCACGACGAGCGCCCCGCATC
                                                                                                      CCGGCCGGCGCCATCTACTTCATGATGGACGAACCCGACGTGCAGCGCATCCTGGCGTTC
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; ORGANISM: Streptomyces refuineus subspecies thermotolerans
US-10-166-087-1
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Best Local Similarity
Matches 474; Conserve
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25131 GCGCAGGTGAAGACGTTCTGCGCCACCGAGGGCATCACCACCGGCATGTTCTTCGCCGCC 25190
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                                                                           TOGCTGGACGCGTATCCCTACGTGGCCGGCTCCACCATGCTCAAGCAGGACCGCGTGCTG
                                                                                                       CAGGACGCGCCCGAGCTGGGCACCGAGGTGACGGCCGACCTGTTCGCCGAGGCCGCCGCG 25850
                                                                                                                                      TTCGGCCGCTCGCGAGACGCTGCCGCTGATCGAGGCCGCCATGGCGCGCCAGGACGTC
                                                                                                                                                                      GCGCGGCGCCTGGAGACGCTCGTGCGCAGCGTGATGGCCGACCCGGACACGGACGTCCGC
                                                                                                                                                                                                 GGCCGCGAGCTGGACGTGCCGGTGGTGATCTCGCACCACGAGGTCATGGGCCAGCCCAAT 810
                                                                                                                                                                                                                                                                                             ACGCTGGTCGTCGAGCACCACCTCGGCCTCGGCCGGCGCGCGAAGCCTCGCGGCGTACCTG
                                                                                                                                                                                                                                                                                                                          ACCACCGAAGAGATCATCGAGGTGTGCCGGCCGCTGAGCGCGCATGGCGGCATCTACGCC
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ilarity 41.9%;
Conservative
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Pred. No. 3.7e-09;
0; Mismatches 658;
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Ouery Match 4.3%; Best Local Similarity 44.6%;

Matches 434; Conservative

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720 CGTGGCCGCGCTGGAGGAAACCTTCCGCATCGGCCGCGAGCTGGACGTGCCGGTGGTGAT 779

GCTGCTGGACGCGGGGGGGGGTGAACGAGGGCAACACCTACGGCGTAACGCCGCTGCA 3350 GCCGCTGAGCGCGCATGGCGGCATCTACGCCACCCACATGCGCGACGAAGGCGAGCACAT 719

CGTGTACGCCAAGAACCAGTGGATCCGCGAGGACGTGCTGCTGCTGCTGCTCGAGCGCGG 3290

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3586 CACGCCGCTGCACGCCTACGTGCAGTACGACGGCGTGCGGCCGGAGGTGGTCGCGCTCAT 352

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480 TTCAACGCTGCGCGCGCGTCATGCCGGACTTGCAGCGCGCCGCCACCGACGAGGAAAT 539

3646 GATCGTGCGCGTGCTGGAGGCCGGTGCGGACGTGAAAGCCAAAGGACTCCTGCGGCCG

3587

360 GCCCGCCCCCTGGACCTGCTGGACGAAGGCGGCTCTTACCGTTTCGAGCGCTTCGCCGA 419

Score 75.8; DB 9; Pred. No. 2.6e-08; 0; Mismatches 527;

Length 4020; Indels

12;

Gaps

420 CTACCTGGACGCGTTGCGGGCCACGCCGGCGGCGGCCGTCAACGCCGCCTGTATGGTGGGGCCA 479

3469

GCTCTCCTTCCTGGCTTTCTGCGGCCCCGACGCGCGAGCTCGAGGTCGCGCGGCT 3410

CGGCGCCTTCTACCCGCCCCCCCCCCCCCCCCCACCACCAAGAGATCATCGAGGTGTGCCG 659 CGCGGCCATGCGGGACCTGGCCGAGGAAGCCATGGCCAGCGGCGCCATCGGCATTTCGAC

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: LENGTH: 4020
: TYPE: DNA
: ORGANISM: Orf virus strain NZ-2
US-09-796-679-5
                                                                                                                                                                                                                     APPLICANT: Robinson, Anthony J
APPLICANT: Lyttle, David J
APPLICANT: Lyttle, David J
APPLICANT: University of Otago
TITLE OF INVENTION: Parapoxvirus vectors
FILE REFERENCE: 23607 MRB
CURRENT APPLICATION NUMBER: US/09/796,679
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/15,421
PRIOR FILING DATE: 1998-09-29
PRIOR FILING DATE: 1998-09-29
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US-09-796-679-5/c
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                                                                            SOFTWARE: PatentIn SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09796679 Publication No. US20030013076A1 GENERAL INFORMATION:
                                                                                                                                        PRIOR APPLICATION NUMBER: NZ 286284 PRIOR FILING DATE: 1996-03-29
                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/N297/00040
PRIOR FILING DATE: 1997-03-27
                                                                                                                             NUMBER OF SEQ ID NOS:
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APPLICANT: Zhao, L.

APPLICANT: Zhao, L.

TITLE OF INVENTION: DNA encoding methymycin and pik

FILE REFERENCE: 600, 438US1

CURRENT APPLICATION NUMBER: US/09/860,846

CURRENT FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: 09/105,537

PRIOR FILING DATE: 1998-06-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1

SEQ ID NO 1
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                                                                                                                  Query Match 4.2%;
Best Local Similarity 43.2%;
Matches 586; Conservative
                                                                                                                                                                                                ORGANISM: Streptomyces venezuelae -09-860-846-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09860846 Patent No. US20020164742A1
                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sherman, D.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT:
                                    4799 GGCGAGGAACTGCGCGCGCGCACCCCGTGTTCGCCGCCGCCCCTCGACACCGTGTACGCG 4858
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Pred. No. 6.3e-08;
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ACCACGGTCGAGGTCGCCGGCGGCGACGGCGTCCTGCTGACCGGCCGTCTCTCCCTGACC 5929
                                                                              ATGACCGGCCTGACCGCCGCGCGCTTCGGC-----CTGGCCGGGCGGCGGGCAGCTGCAG 1302
                                                                                                                                             GGGCAC----TATGCGCGCGACCTGGGCCTGTTCCCGCTGGAGACGGCGGTATGGAAG
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APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and
FILE REFERENCE: 600.536GS1
CURRENT APPLICATION UNMER: US/09/988,384B
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: PCT/US99/14398
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,537
PRIOR APPLICATION NUMBER: US 09/105,537
PRIOR APPLICATION NUMBER: US 09/105,537
PRIOR PILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 53
SEQ ID NO 1
TENCENT: 15872
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US-09-988-3848-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.2%;
Best Local Similarity 43.2%;
Matches 586; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09988384B Publication No. US20030073824A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sherman, D.H. APPLICANT: Liu, H.
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GCCGAGGTCGTCGAGTCCCTGAAGGGCTACGAGGGCAGGGTCGCCGTCGCCGCCGTCAAC
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Pred. No. 6.3e-08;
0; Mismatches 747;
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AGCGGCGACGGCGAGTCGCCGGGCGCGCACCTTCG 6146
                             GCCGCCTGAGCCCGGCGCCAGCCCTTACAATCCGGCG
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Sequence 1, Application US/09861289
Patent No. US20020110897A1
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
APPLICANT: DNA encoding met)

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RESULT 13 US-09-861-289-1

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; ORGANISM: Streptomyces venezuelae
US-09-861-289-1
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Best Local Similarity 43.2%;
Matches 586; Conservative
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CURRENT APPLICATION NUMBER: US/09/861,289
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
5570 GTCCTCACGGCACTCGCCGAGGAGGCTCTCGCGCCCGGCACGGACGCCCCGGACGCCCGG
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                                                                                                          GCCGGCTCCACCATGCTCAAGCAGGACCGCGTGCTGCTGGCCGGACGCACCATCATCACC
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                                    TGGTGCAAGCCCTTCCCCGAACTGAGCGGGCGCGACCTGGATGAAGTCGCGGCCGAGCGC
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Pred. No. 6.3e-08;
0; Mismatches 747;
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; TYPE: DNA
; ORGANISM: HERPES VIRUS,
US-09-825-288A-1
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Best Local Similarity 42.6%;
Matches 581; Conservative
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                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/825,288A CURRENT FILING DATE: 2001-04-02 PRIOR APPLICATION NUMBER: 09/259,821 PRIOR FILING DATE: 1999-03-01 PRIOR APPLICATION NUMBER: 08/690,473 PRIOR FILING DATE: 1996-07-26 NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LEOPARDI, ROSARIO
APPLICANT: ROIZMAN, BERNARD
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4
FILE REFERENCE: ARCD:317USC1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1075 ATGGACGAACCCGACGTGCAGCGCATCCTGGCGTTCGGCCCGACCATGATCGGCTCCGAC
                                                                                                                                         189 GGTCGACGTGTCGGGCCTGGTCGCGCCCCGGCTTCATCGACTCGCACACCCACGACGA 248
                                                                  CAACTACCTGCTCAGGCGTCGCGACATGACGCCCAAGATCTCGCAGGGCGTCACCACGGT 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCCTGGAGCTCGCCCTCGCGGCGGCGACCACGTCGGGGCGGTCCGGGTGGAGGAACTC
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AGCGGCGACGGGGCGGCGCGCGCGCCACCTTCG 6146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCGCCTGAGCCCGGCGCCAGCCCTTACAATCCGGCG 1516
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                                                                                                                                                                                                                                                                                                                                          2.1
                                                                                                                                                                                                                                                                   TYPE 1
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                                                                                                                                                                                           Score 73.4; DB 9;
Pred. No. 8.9e-08;
                                                                                                                                                                            Mismatches 766;
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                                   CGAGCGCGCCGCCATCCATTCCGTGTACGTCAACGGCGCGCCGGTCTGGCAAGAGCA 1436
                                                                                                                                                                                       CGCCGCGCTTCGGCCTGGCCGGGCGCGGCAGCTGCAGGCCGGGTACTTCGCCGACCT
                                                                                                                                                                                                                                                                TGCGCGCGACCTGGGCCTGTTCCCCGCTGGAGACGGCGGTATGGAAGATGACCGGCCTGAC
                                                                          GGTGGTGTTCGACCCGGCCACGGTGGCCGATAC----CGCCACCTTCGAACACCCTAC
                                                                                                                                                     GECGECCGCCGCCTCCGCCGCGCGCGCGGAGGGGCGCAAGCCCAAGAGTCCCGGCCC
                                                                                                                                                                                                                                                                                                                                           GCACGACGAGCGCCCGCATCCGCGCCTGTGGGGCACCTTCCCGCGGGTGCTGGGGCACTA 1202
                                                                                                                                                                                                                                                                                                                                                                                CCAGAGCCTGCGCCCCTGCTGGCGGCGGCGGCCAGCGCACCGGACGCCGACGCGCT 2501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCCTTCCCCGAACTGAGCGGGCGCGACCTGGATGAAGTCGCGGCCGAGCGCGAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTGTT06CGCGCGAGAACGCGGCGCTGACGGGGGGCCGCGGGGAGCCCCGGGGGCGCGC 1847
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US-09-815-242-4056
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 201-02-16
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US-09-815-242-4056
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                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.1%;
Best Local Similarity 43.8%;
Matches 371; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version SEQ ID NO 4056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/815, CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR EILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4056,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA, 011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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256 CTGCTCAGGCGTCGCGACATGACGCCCAAGATCTCGCAGGGGGTCACCACGGTGGTCACG
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                                                                                                                                               439
                                                                                                                                                                   136 GECGACCGCATCGCCATCGGCGATCTGTCGGACGCCGCGCGCACACCCCGGGTCGAC 195
                                                                                                                                                                                                                        379
                                                                                                                                                                                                                                                                                 319 GTGCAGGTGCAGAACCGCGTCACCCGGGACCGAGCCGGAAGCTCCCGGGAAGAAGTGACCCCGG 378
                                                                                                                                                                                                                                                                                                                     16 GCGGAAGGAGATTTCCATGTCCCAATCCGATTCCCAGCCCTTCGACCTGCTGCTCGCG 75
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                                                                                      GTGTCGGGCCTGGTGGTCGCGCCCGGCTTCATCGACTCGCACACCCACGACGACAACTAC 255
                                                       GAACTGGCCGCCTCGACGGCGTCGGCGACGTCCAGTTGTTCGGCCTCGGCGACTATTCG
                                                                                                                                CCGGATAACCGCTACGACATGCTCTACCTGTCGAACTACGCGGTGCTCAACGTGAAGGAC
                                                                                                                                                                                                                                            CTCGGCATCACCGTCGACAAGGCCTCGCCCGACCTGACCATGGTCGTGCACCTGACCTCG 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGCCCTTACAATCCGGCGTGAACGGGGGGGGGGTGCCGCCCCT 1541
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Xu, H. Howard
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                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 471;
                                                                                                                                                                                                                                                                                                                                                                                    Score 72.4; DB 10;
Pred. No. 1.5e-07;
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1153 GTGATGCA 1160
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                                                                                                                                                                                                                                             736 GAAACCTTCCGCATCGGCCGCGAGCTGGACCTGCCGGTGGTGATCTCGCACCACAAGGTC 795
                                                         856 GCGCGCCA 863
                                                                                                                                                                                      796 ATGGGCCAGCCCAATTTCGGCCGCTCGCGCGAGACGCTGCCGCTGATCGAGGCCGCCATG 855
                                                                                                                                                                                                                                                                                                                                                                             979 TCCATCGTCTACGACCCGACCATCTTCGTCCGCGG------CTCCATCGAGGCGGTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         496 GCGGTCATGCCGGACTTGCAGCGCGCCGCCCACCGACGAAATCGCGGCCATGCGGGAC 555
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